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Mar 25 02:47

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:48:13 1997; MasPar time 60.19 Seconds 205.147 Million cell updates/sec

Tabular output not generated.

Description: Title: >US-08-644-289-3 (1-28) from US08644289.seq

N.A. Perfect Score: Sequence: 28 1 AGTCGAATTCATTGGGACCATCCTGGCT

28

TCAGCTTAAGTAACCCTGGTAGGACCGA

Scoring table: TABLE default

Gap

Mmatch STD: Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST17 12:EST12 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST33
23:EST33 34:EST34 35:EST29 30:EST30 31:EST31 32:EST33
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST55 53:EST53 54:EST45 55:EST55 56:EST56
67:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST66
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST71 78:EST78 79:EST79 37:EST80
81:EST81 82:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98 1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

99:EST99
99:EST-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

Database:

141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 156:gnEST15 156:gnEST1 158:gnEST15 156:gnEST15 157:gnEST1 158:gnEST2 159:gnEST3 160:gnEST6 163:gnEST6 163:gnEST7 164:gnEST8 165:gnEST9 166:gnEST9 167:gnEST1 168:gnEST1 168:gnEST1 169:gnEST13 170:gnEST14 171:gnEST15 172:gnEST16 173:enSTS1 174:enSTS2 136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1 130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7

Statistics: Mean 7.030; Variance 1.506; scale 4.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

Query

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42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	ហ	4	ω	2	_	No.
16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	17	17	17	17	17	18	18	18	18	19	Score
57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	60.7	60.7	60.7	60.7	60.7	64.3	64.3	64.3	64.3	67.9	Match
515	494	449	447	439	433	432	428	428	427	427	424	419	414	411	407	407	402	365	359	354	347	344	330	319	296	285	284	252	225	215	202	443	443	386	341	197	509	473	457	430	410	Match Length
52	70	18	128	67	ည	55	67	159	106	65	36	86	67	22	28	26	99	104	21	117	24	174	49	142	30	105	138	105	39	163	164	67	157	72	105	128	17	34	86	115	62	DB
N20867	N76766	Н39611	T97624	N66945	н87153	N29941	N68188	HS156315	T17269	N59638	н97697	R90920	N67592	H53579	H70615	н65947	R93365	T05261	H50664	T59311	H58307	HSA152WC5	HUM418C11B	N84245	н78195	T11542	HUMUT854A	T10560	HSC0KC122	HS 611312	HS 681308	N69020	HS020330	R02746	T11785	T99302	H38514	H90484	R89652	52	N51985	ID
.sl Homo	.rl Homo	.rl Homo	5.sl Homo	za48d11.s1 Homo sapie	Homo	yw53c06.sl Homo sapie	Homo 6	<ol><li>1.rl Homo sap</li></ol>	Homo sap	.si Homo	.sl Homo	.sl Homo	.sl Homo	yq87c08.sl Homo sapie	Homo	yul5bl2.sl Homo sapie		omo	yp86e04.sl Homo sapie		sapie	piens (	Human fetal brain cDN	KK6769F Homo sapiens	yu84ell.sl Homo sapie	ens	STS UT854, 5'	bc022 Ноπ	partia	s1 Homo	1 Hom	Ното	Ноп	.sl Homo sapi	sap	rl Homo	rl Homo	.rl Homo	1 Homo s	1.sl Homo	yz07f07.sl Homo sapie	Description
	2.27e-02	2.27e-02	2.27e-02	2.27e-02		R 3	2.2	2	2.27e-02	2.27e-02	.27e-0	2.27e-02	•	2.27e-02	2.27e-02	2.27e-02	2.27e-02	2.27e-02		2.27e-02	2.27e-02	2.27e-02	2.27e-02	2.27e-02	2.27e-02			2.27e-02	2.27e-02	~	~	<u>.</u> -	_	1.41e-03	1.41e-03	1.41e-03	7.88e-05	7.88e-05	7.88e-05	7.88e-05	4.01e-06	Pred. No.

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# 43 16 57.1 550 62 N50065 yz10h03.s1 Homo sapie 2.27e-02 c 44 16 57.1 578 34 H93071 yv06h04.s1 Homo sapie 2.27e-02 c 45 16 57.1 1953 151 W18192 IMAGE:20083 Soares in 2.27e-02

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187

# ALIGNMENTS

NID RESULT LOCUS KEYWORDS ORIGIN BASE COUNT FEATURES COMMENT REFERENCE SOURCE ACCESSION DEFINITION TITLE ORGANISM JOURNAL AUTHORS source N51985 N51985 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Unpublished Hillier, L., Clark, N., Dubuque, T., Homo sapiens sclerosis 2NbHMSP vector=pT7T3D (Pharmacia) with a modified polylinker V\_TYPE: phagemid host=DH10B (ampicillin resistant) g1193151 yz07f07.sl Homo sapiens cDNA clone 282373 3' similar to contains This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. High quality sequence stops: 188 Contact: Wilson RK The WashU-Merck EST Project Unpublished (1995) Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Dr. Kevin G. Becker (NINDS/NIH). multiple sclerosis lesions from one patient was kindly provided by constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 through one round of normalization to a Cot = 5. Library RI sites of a modified pT7T vector (Pharmacia). Library went human clone=282373 primer=m13 -40 forward library=Soares multiple Alu repetitive element; contains element LTR1 repetitive element ;. Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu WashU-Merck EST Project Wilson, R. Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. double-stranded cDNA was size selected, ligated to Eco RI adapters Rsitel=Not I Rsite2=Eco RI 46 year old male, 1st strand cDNA was (Pharmacia), digested with Not I and cloned into the Not I and Eco (bases 1 to 410) : 314 286 1800 : 314 286 1810 103 ۵ <1..>410 /note="human" /organism="Homo sapiens" /clone="282373" 1..410 Location/Qualifiers 108 c 410 bp 88 g 109 t Elliston, K., Hawkins, M., EST 2 others MO 63108 14-FEB-1996

Query Match 67.9%; Best Local Similarity 84.6%; Matches 22; Conservative

Score 19; DB 62; Length 410; Pred. No. 4.01e-06; 0; Mismatches 4: Indala

<u>.</u>.

Gaps

0

DEFINITION

R89652

457 bp

mRNA

24-AUG-1995

ym97d01.rl Homo sapiens cDNA clone 166849 5' similar to contains

Alu repetitive element; contains MER22 repetitive element; R89652

Mar 25 02:47 US-08-644 289:3.rst

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မှ 밁 ORIGIN COMMENT DEFINITION RESULT BASE COUNT FEATURES REFERENCE SOURCE KEYWORDS ACCESSION FOCUS Query Match 64.3%; Best Local Similarity 100.0%; ORGANISM Matches AUTHORS source 186 agccaggatggtcccaat 203 28 AGCCAGGATGGTCCCAAT 11 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., vector=pBluescript SK- host=SOLR cells (kanamycin resistant) primer=-2lml3 Rsitel=Eco81 Rsite2=KhoI Placental tissue from a Caucasian male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.2 kb; Uni=ZAP XR Vector; 5' adaptor sequence: 5'-GANTTCGGCACGAG-3', 3' adaptor sequence: High qality sequence stops: 353 Source: IMAGE Consortium, LLNL Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project Homo sapiens element. ya72a11.s1 Homo sapiens cDNA clone 67196 3' 4444 Forest Park Parkway, Box 8501, St. Louis, Washington University School of Medicine Contact: Wilson RK Unpublished (1995) Eutheria; Primates; Catarrhini; Hominidae; Homo. 5'-CTCGAGTTTTTTTTTTTTTTTTT-3'. human clone=67196 library=Stratagene placenta (#937225) g654499 T52639 T52639 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Email: est@watson.wustl.edu Fax: 314 286 1810 Tel: 314 286 1800 WashU-Merck EST Project Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; 18; (bases 1 to 430) 91 Conservative ø /note="human' /clone="67196" Location/Qualifiers /organism="Homo sapiens" 1..430 119 с 430 bp Score 18; DB 115; Pred. No. 7.88e-05; 104 g 112 t DB 115; Length 430; 4 others Indels contains Alu repetitive MO 63108 0: 08-FEB-1995 Gaps 0

REFERENCE AUTHORS Ş 뭐 ORIGIN BASE COUNT FEATURES COMMENT SOURCE KEYWORDS UID TITLE JOURNAL Query Match 64.3%; Best Local Similarity 87.5%; ORGANISM Matches source 172 gaatgcagtggcaccatcctggct 195 5 GAATTCATTGGGACCATCCTGGCT 28 g954479 EST. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Contact: Wilson RK WashU-Merck EST Project Unpublished (1995) Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Hillier, L., Clark, N., Dubuque, T., Homo sapiens representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues human clone=166849 library=Soares adult brain N2b4HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 457) Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; midbrain, pons and medulla. subcortical white matter, basal ganglia, thalamus, cerebellum, RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL High quality sequence stops: 303 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; constructed by Bento Soares and M.Fatima Bonaldo. The adult brain double-stranded cDNA was size selected, ligated to Eco RI adapters oligo(dT) primer [5" IMAGE Consortium (info@image.llnl.gov) for further information. Email: est@watson.wustl.edu 55-year old male. (Pharmacia), digested with Not I and cloned into the Not I and 314 286 1810 92 314 286 1800 Conservative Ø <1..>457 /organism="Homo sapiens" /clone="166849" /note="human" Location/Qualifiers 123 c 1st strand cDNA was primed with a Not I -Score 18; DB 98; Pred. No. 7.88e-05; 0; 103 Mismatches g 130 t Elliston, K., Hawkins, M., <u>ω</u> Length 457; 9 others Indels MO 63108 0; Gaps 0; Eco

RESULT

ACCESSION DEFINITION

Alu repetitive element; contains THR repetitive element; H38514

yp69b12.rl Homo sapiens cDNA clone 192671 5' similar to contains

16-AUG-1995

H38514

509 bp

# Mar 25 02:47 US-08-644-289-3<sub>.ESE</sub>

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မှ ORIGIN BASE COUNT COMMENT Locus RESULT FEATURES REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION Matches Query Match 64.3%; Best Local Similarity 87.5%; ORGANISM JOURNAL AUTHORS source 94 agccaggatggtgccactgcattc 117 28 AGCCAGGATGGTCCCAATGAATTC 5 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. Alu repetitive element;. H90484 High quality sequence stops: 371 WashU-Merck EST Project Homo sapiens cDNA was ligated to Eco RI adaptors (Pharmacia), g1080914 yv01g06.rl Homo sapiens cDNA clone 241498 5' similar to contains H90484 This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL Tel: 314 286 1800 Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine Contact: Wilson RK Unpublished (1995) The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver human clone=241498 primer=M13RP1 library=Soares fetal liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker Email: est@watson.wustl.edu ∦ilson,R. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; cDNA was primed with a Pac I - oligo(dT) primer [5' and spleen from a 20 week-post conception male fetus. 1st strand 21; [MAGE Consortium (info@image.llnl.gov) (bases 1 to 473) 131 Conservative മ <1..>473 a 74 c /note="human" /clone="241498" /organism="Homo sapiens" 1..473 Location/Qualifiers 473 bp Score 18; DB 34; Pred. No. 7.88e-05; <u>.</u> 113 g Mismatches 152 t for further Length 473; 3 others Indels digested with Pac 28-NOV-1995 0 Gaps 0;

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REFERENCE
AUTHORS
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holman, M., Hultman, M., Kucaba, T., Le, M., Lennor Parsons, J., Rifkin, L., Rohlfing, T., Soares, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier, L., Clark, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              midbrain, pons and medulla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subcortical white matter, basal ganglia, thalamus, cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aortic aneurysm. RNA was prepared from a pool of tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human clone=192671 library=Soares adult brain N2b4HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI
  T99302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by Bento Soares and M.Fatima Bonaldo. The adult brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    through one round of normalization to a Cot = 53. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded cDNA was size selected, ligated to Eco RI adapters
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/clone="192671"
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                                                                                                                                                                                                                               Pred. No. 7.88e-05;
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                                                                                                                                                                                                                                                     Length 509;
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31-MAR-1995
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                                                                                                                                                                                                                                                                                           60.7%;
Best Local Similarity 83.3%;
Matches 20; Conservative
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JOURNAL
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g596489
EST.
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                                                                                          All38R Homo sapiens cDNA clone All38 similar to Alu repetitive
                                                                                                                  T11785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High qality sequence stops: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I and cloned into the Pac I and Eco RI sites of the modified pT7T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               considered overall poor quality.
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                                                                                                                  341 bp
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Pred. No. 1.41e-03;
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Best Local Similarity 100.0%;
JOURNAL
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                                                                                                                                                                                                                                                     cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
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Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
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Unpublished (1995)
                                                           Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                             Hillier, L.,
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                           Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dI) primer (5')
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Liew CC
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                    The WashU-Merck EST Project
                                                                                                    Holman, M., Hultman, M., Kucaba, T.,
                                                                                                                                                                        Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                     constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                               vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
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                                                                                                                                                 (bases 1 to 386)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        liewcc@utcc.utoronto.ca.
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a 96 c
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                                                                                                                        Clark, N., Dubuque, T.,
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                                                                                                    Le, M., Lennon, G., Marra, M.,
                                                                                                                          Elliston, K., Hawkins, M.,
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Best Local Similarity 84.0%;
Matches 21; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N69020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-1996 (Rel. 47, Last updated, Version 1) za7lel1.s1 Homo sapiens cDNA clone 298028 3' similar to contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
Sequence 443
                                                                                                                 source
                                                                                                                                                               Key
                                                                                                                                                                                                                            est@watson.wustl.edu High quality sequence stops: 340 Source: IMAG
Consortium, LLNL This clone is available royalty-free through LLNL
                                                                                                                                                                                                                                                                            School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK WashU-Merck EST Project Washington University
                                                                                                                                                                                                                                                                                                                                                  Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Holman M., Hultman M., Kucaba T., Le M., Lennon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                        "The WashU-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                              Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                      Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-1996 (Rel. 47,
                                                                                                                                                                                   contact the IMAGE Consortium information. NCBI gi: 1225181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 286 1810
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BP; 100 A; 108 C; 89 G; 145 T; 1 other;
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/note="human"
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                                                                                           /organism="Homo
                                                                                                                                                               Location/Qualifiers
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Query Match 60.7%; Best Local Similarity 100.0%;

Score 17; DB 157; Pred. No. 1.41e-03;

Length

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17;

Conservative

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328 gccaggatggtcccaat 344

27 GCCAGGATGGTCCCAAT 11

SOURCE KEYWORDS NID ACCESSION DEFINITION

g1225181 EST.

Alu repetitive element;.

za7le11.s1 Homo sapiens cDNA clone 298028

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AC OC SERVER OF THE SERVER OF မှ 밁 Matches Query Match 57.1%; Best Local Similarity 86.4%; HS 681308 04-APR-1996 (Rel. 47, Created)
05-APR-1996 (Rel. 47, Last updated, Version zb14f11.s1 Homo sapiens cDNA clone 302061 3' mRNA 04-APR-1996 (Rel. 47, Created)
05-APR-1996 (Rel. 47, Last updated, Version zb03c03.sl Homo sapiens cDNA clone 300964 3' N80681; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., EST. Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wils Trevaskis E., Waterston R., Williamson A., "The WashU-Merck EST Project"; Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Homo sapiens (human) N79611; HS611312 Sequence source ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. NCBI gi: 1243382 est@watson.wustl.edu High quality sequence stops: 163 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL School of Medicine 4444 Forest Park Parkway, Box 85 MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University Unpublished. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae Homo sapiens (human) Theria; "The WashU-Merck EST Project"; 152 ccagcatggtcccactgaagtc 173 26 CCAGGATGGTCCCAATGAATTC 5 Eutheria; Primates; Haplorhini; Wilson 202 BP; 37 A; 82 C; 40 G; 42 T; 1 other; standard; RNA; EST; standard; RNA; EST; Conservative RK WashU-Merck EST Project Washington University 1..202Location/Qualifiers <1..>202 /note="human" /clone="300964" /organism="Homo sapiens" Score 16; DB 164; Pred. No. 2.27e-02; 0 202 Mismatches ВP DB 164; Length 202; Catarrhini; Wohldmann P., Wilson 2) Box 8501, Indels Hominidae Hominidae P., Wilson St. Louis, 0; Gaps R.

0

REFERENCE

(bases 1 to 443)

ORGANISM

Homo sapiens

RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library

host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI 19 human clone=298028 primer=m13 -40 forward library=Soares fetal lung

1st strand cDNA was primed with a Not I - oligo(dT)

with a modified polylinker

week fetus.

NbHL19W vector=pT7T3D (Pharmacia)

double-stranded cDNA was size selected, ligated to Eco RI adapters

(Pharmacia), digested with Not I and cloned into the Not I and Eco

constructed by Bento Soares and M.Fatima Bonaldo.

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

JOURNAL

Unpublished (1995)

The WashU-Merck EST Project

Washington University School of Medicine

Forest Park Parkway,

Box 8501, St. Louis,

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Contact: Wilson RK WashU-Merck EST Project

BASE COUNT ORIGIN

100

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89

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145 t

others

<1..>443

/note="human" 108 c

Query Match 60.7%; Best Local Similarity 100.0%;

Conservative

Score 17; DB 67; L Pred. No. 1.41e-03; 0; Mismatches 0;

Length 443;

Indels

0

Gaps

0

FEATURES

Location/Qualifiers

IMAGE

clone is available royalty-free through LLNL; contact the E Consortium (info@image.llnl.gov) for further information.

Source: IMAGE Consortium, Email: est@watson.wustl.edu

TINI

quality sequence stops: 340

source

/organism="Homo sapiens" /clone="298028"

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GCCAGGATGGTCCCAAT 11

328 gccaggatggtcccaat 344

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Best Local Similarity 86.4%;
                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 215 BP; 42 A; 86 C; 41 G; 44 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRNA
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F01978
                                                                                                                                 Cloning method: total mRNA was oligo-(dT) primed and directionally cloned \bar{5}' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                  C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
                                                                                                                                                                                                                                               Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                 Primer: (-21)M13_universal;
                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            partial cDNA sequence; transcribed sequence fragment.
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  Normalization method: Bento Soares, P.N.A.S in
                       Stretch_removed:
                                          cDNA sequence complementary to mRNA (3'end)
                                                                                      Sequencing_method: single read,
                                                                                                                                                                                                                            IMAGE: Integated molecular analysis of the human genome and its
                                                                                                                                                                                                                                                                                                                                                                                     The Genexpress cDNA program
                                                                                                                                                                                                                                                                                                                                                                                                              Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
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                     removed at sequence 5'end
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                                                                                      full automatic;
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Сþ ORIGIN FEATURES SOURCE ACCESSION TOCUS 망 ORIGIN BASE COUNT REFERENCE KEYWORDS DEFINITION FEATURES Matches Query Match 57.1%; Best Local Similarity 94.4%; TITLE Query Match 57.1%; Best Local Similarity 94.4%; JOURNAL AUTHORS ORGANISM source source 34 28 AGCCAGGATGGTCCCAAT 11 agccaggatggtctcaat 51 T10560 T10560 hbc022 Homo sapiens g390714 A molecular inventory of human pancreatic islets:sequence analysis Bell, G.I. and Takeda, J. Human clone-hbc022 library=Human pancreatic islet vector=Lambda ZAPII primer=SK primer Rsitel=Eco RI Rsite2=Xho I mRNA was prepared Email: g-bell@uchicago.edu. 5841 S. Maryland Ave., MC1028, Chicago IL 60637 Tel: 3127029116 Univ. of Chicago Contact: Bell GI or Takeda J Hum. Mol. of 1000 cDNA clones Eutheria; Primates; Catarrhini; Hominidae; Homo. Genexpress\_sequence\_idt: a1c-0kc12. Fax: 3127020271 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; from the Xho I in the vector to the EcoRI site. cDNA was fractionated to remove sequences <1000 bp in size. from normal adult human islets. cDNA was directionally synthesized Genexpress\_library\_idt: C; (bases 1 to 252) 52 a 59 Conservative Conservative Homo sapiens cDNA clone hbc022 5'end. മ /note="Human" /clone\_lib="normalized infant brain cDNA from B.Soares, Psychiatry Dept. Columbia University USA" Location/Qualifiers /isolate="muscular atrophy patient" 56 c 43 g 67 t /organism="Homo sapiens" /clone="hbc022" Genet. /dev\_stage="3 months old" /tissue\_type="total brain" /sex="female" organism="Homo sapiens" ocation/Qualifiers 70 c 252 bp 2, 1793-1798 Score 16; DB 105; Pred. No. 2.27e-02; Score 16; DB 39; Pred. No. 2.27e-02; 0; Mismatches 0; Mismatches 43 g 63 mRNA g (1993)67 t Length 225; Length 252; Indels 0; °, Gaps Gaps 0; **?**:

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39

agccaggatggtctcaat 56

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CP 28 AGCCAGGATGGTCCCAAT 11

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BASE COUNT
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ORGANISM
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AUTHORS
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                                                                              Query Match 57.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                 primer_bind
                                                                                                                                                                                                                                                                                                 source
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMUT854A 284 bp DNA
Human STS UT854, 5' primer bind
L31251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer A:
Primer B:
                                                                                                                                                                                                                                                                                                                                                        Cycles Denaturation Annealing Extension 5 C 10 sec. 62 C 10 sec. 72 C 20 sec. 31 S C 10 sec. 72 C 20 sec. Mg++: 1.25 mM Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tagged sites from the human genome
Unpublished (1994) See COMMENT for author address
Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

1 (bases 1 to 284)

1 (bases 1 to 284)

1 (bases, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                          Alleles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       End to Label: Primer B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetic and physical mapping of simple sequence repeat containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Denaturation: 94C 300sec
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4..22
                                                                                                                                                                                     /evidence=experimental
47 c 91 g
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTCAGGAGATTGAGACC
                                                                              Score 16; DB 138; Length 284; Pred. No. 2.27e-02; 0; Mismatches 1; Indels
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                                                                                  Gaps
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10 sec.
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Search completed: Tue Mar 25 02:49:22 1997 Job time : 69 secs.

Mar 25 02:41 US-08-644-289-2.rng

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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* (MT)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:42:30 1997; MasPar time 10.59 Seconds 312.999 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-08-644-289-2 (1-38) from US08644289.seq 38

N.A. Sequence: 1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 TCAGTCCGGAATCTCAATTTCCTACGGGTACGATGTCT

Scoring table: TABLE default Gap 10

Gap

Nmatch STD: Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.939; Variance 3.336; scale 1.780

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		C		Result
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19	19	26	34	1
50.0	50.0	63.2	100.0 89.5	% Query Match
1181	471 984	91	38 1173	Query Match Length DB
15	: = =	99	21 12	DB BG
Q97854	471 11 Q62363 984 11 Q62361	Q51746 Q51746	T10486 Q67883	ID
Human p53 cDNA.	Fragment coding f	Oligonucleotide p	Human wild-type p Murine p53 DNA.	Description
	for h			
2.07e-01 2.07e-01	2.07e-01 2.07e-01	1.47e-05 2.46e-04	2.73e-13 1.19e-10	Pred. No.

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T14600 T11593 N71089 N71089 N60937 N81478 N60936 Q39093 N71090 T09341 T18877	06/844 067864 067863 027944 067863 027944 027899 092901 092900 092900 092900 09399 092900 09399 092900 073391 073391 073393 041173 041173 041173 074450 074450 074459	US-08-6 129719 022995
pXJCL-hGM-CSF express Babesia sp. oligonucl Sequence of human gra Plasmid pBRVZ insert Sequence encoding hum Plasmid pBRG4 insert Streptomyces nodosus Sequence of human gra Tobacco mosaic virus Protease gene. Human TCL-1 gene.	Human p53 DNA. Vaccinia H6 promoter/ Vaccinia H6 promoter/ Vaccinia H6 promoter/ Vaccinia H6 promoter/ Mutant p53 polypeptid Mixed oligonucleotide Base substituted roco MoMIV gag matrix proto MoMIV gag matrix proto MoMIV mutated gag mat MoMIV mutated gag mat MoMIV mutated gag mat MoMIV mutated gag mat MoMIV gag/pol gene pr Human Natriiretic Pep Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF1. Hybrid vector pSF-MDR Retroviral vector MFC Novel AMP/MOF virus c myoD retroviral expre MoMIV gag/pol gene re Vector M48 used for g myoD retroviral expre Vector M48 used for g myoD retroviral expre	JS-488-644:289-2.rng 9719 Wild type p53 gene se 2995 Sequence encoding 53
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## ALI GNMENTS

S	റ്റ	S	Sd	PΤ	PΤ	PT	DR	ΡI	PA	PR	Эď	PD	PN	SO	X	X.	¥	Æ	DΤ	AC	ID	RESULT
gene. An epitope from intron 10 of the human p53 gene is used to	N-terminal (nucleotides -111 to 1090) portion of the wild-type p53	T10486-T10488 are primers used in a RT-PCR reaction to obtain an	Disclosure; Page 7; 40pp; English.	individual treatment regimes.	useful in diagnosis or prognosis of cancer, and for establishing	New antibodies specific for alternatively spliced mammalian p53 -	WPI; 96-140137/15.	Kulesz-Martin MF;	(HEAL-) HEALTH RES INC.	14-JUN-1994; US-259612.	05-JUN-1995; 150994.	15-DEC-1995.	CA2150994-A.	Homo sapiens.	reverse transcriptase polymerase chain reaction; ss.	proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle;	Tumour suppressor; p53; alternative splicing; antibody; cancer;	Human wild-type p53 gene N-terminal sense RT-PCR primer.	03-OCT-1996 (first entry)	T10486;	T10486 standard; DNA; 38 BP.	LT 1

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RESULT RESULT PROCESS OF PROCESS 
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                                                                                                                                                                                                                                   using primers MM082 and MM083 and plasmid pl1-4 as a template. The 129 bp amplified fragment contains the 3' end of the H6 promoter, the 5'-most bases of the murine p53 gene, and 15 bp which overlap fragment III. Fragment III was produced using primers MM084 and MM085 and plasmid pl1-4 as a template. The 301 bp amplified fragment contains the 3' end of the p53 gene, and the 5' end overlaps fragment II. The three PCR products were pooled and primed with MM080 and MM085. The resultant 588 bp fragment contains a BamHI site followed by H6 promoted p53. This was inserted into pNC5LSP5 to generate plasmid pMM148 containing H6 promoted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         murine; interleukin-2; II-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector; plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; polymerase chain reaction; poxvirus; pSD542; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the wildtype murine p53 gene from the translation initiation codon to the stop codon. This sequence was used in the construction of an ALVAC-based recombinant virus containing the wild-type murine p53 gene. Three PCR fragments were generated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JT 2
Q67883 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spliced p53. The antibodies are useful in the diagnosis and prognosis of human cancer and in the study of p53 and alternatively spliced p53
                                                                                                                                                                           between
                                                                                                                                                                                                         wildtype murine p53 in the ALVAC C5 insertion locus. Recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as a template. The 228 bp amplified fragment contains the Hb promoter and the 5'-most bases of the murine p53 gene. Fragment II was produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragment I was produced using primers MM080 and MM081 and plasmid pRW825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding cytokine and/or tumour associated antigen Example 31; Fig 38; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q67883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells they may cause cell cycle arrest. Vectors contg. p53as cDNA may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              create antibodies directed against this sequence in an alternatively
                                                              an antigenic or immunological response, ie. for immunisation against
                                                                                                                                    virus vCP263, which contains the vaccinia H6 promoted murine p53 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 94-263767/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cox WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1994; U00888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used in gene therapy of
                                    pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9416716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen; human; interferon; IFN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine p53 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (p53as) and their expression. When the antibodies are injected into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoletti E, Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                     this donor plasmid and ALVAC rescuing virus produced recombinant
1173 BP;
                                                                                                   The resulting virus may be used in a composition for inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The 228 bp amplified fragment contains the H6 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 A;
279 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancers and other proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 21;
Pred. No. 2.73e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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349 C;
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304 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
241 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RESULTING AND ACCORDANCE SERVICE STREET STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1028 aggccttagagttagaggatgcccatgctacaga 1061
                                                                                                                                                               Shank DD,
                                                                                                                                                                                                                     24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                           01-DEC-1993.
                                                                                                                                                                                                                                                                                                    EP-571911-A.
                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q51746 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be useful as an initial screen for mycobacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shank DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q51746 standard;
  Oligonucleotide probe
                       Claim 3; Page 14; 23pp; English.
                                                        samples
                                                                             detection and amplification of Mycobacteria nucleic acid
                                                                                                         New oligo:nucleotide probes specific for Mycobacteria -
                                                                                                                                     WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligo:nucleotide probes specific for Mycobacteria - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1993;
                                                                                                                                                                                           (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BECT ) BECTON DICKINSON CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                               Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spears PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.4%;
0.0%;
MK14-A consists of nucleotides 5-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 9; I
Pred. No. 1.47e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.19e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                               in
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  K14
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                                                                                                           for
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                                                                                                                                                                                                                                                            50.0%;
Best Local Similarity 82.8%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                       T 6
Q62361 standard; cDNA; 984
                            062361;
                                                                                                                                                                                                                                                                                                                                                                                          each of these fragments.
Sequence 471 BP; 128 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-radioactive detection of p53 specific antibodies — on immobilised p53 or its fragments, then reaction with second antibody, for diagnosis of tumours and suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein R, Schranz P, WPI; 94-135732/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 5
Q62363 standard;
     18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region. Preferred fragments contain amino acids 1-241, 40-349,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies specific for p53 are detected by binding to immobilised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 25; 35pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              second antibody, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R51878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1993; E02666.
30-SEP-1992; DE-232823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09408241-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contain start or stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragment coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            062363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    368-386.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= p53(237-393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-oncogene; cancer; tumour; antibody binding region; epitope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 TCTGTAGCATGGGCATCCTTTAACTCTAAGGCCT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 hhvvhhvhvsvvvvhhvvhhvhyhvyvsvct 62
                                                                                                                                                                        AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                                                                                                                                                             aggccttggaactcaaggatgcccaggct 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            partial CDS, therefore sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or . See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 1..471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for human p53 amino acids 237-393.
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5.9%;
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Pred. No. 2.46e-04;
27; Mismatches 5
                                                                                                                                                                                                                                                                                                           Pred. No. 2.07e-01
                                                                                                                                                                                                                                                                                                                                        Score 19;
                                                                                                                                                                                                                                                                                 ç
                                                                                                                                                                                                                                                                                                                                                                                          133 C;
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volkmann M,
                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              does
                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reaction with and suitable !
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                                                                                                                                                                                                                                                                                                                                     Length 471;
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                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity 82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               each of these fragments.
Semmence 984 BP; 224 A;
              Klein R, Schranz
WPI; 94-135732/16.
                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG. Klein R, Schranz P, Tessmer C, Volkmann M,
                                                         30-SEP-1993; E02666.
30-SEP-1992; DE-232823.
                                                                                                                                                                                                                                                       Human nuclear
                                                                                                                                                                                                                                                                                                               Q62359 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 24; 35pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   second antibody, for diagnosis of tumours and suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on immobilised p53 or its fragments, then reaction with labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-radioactive detection of p53 specific antibodies - by capture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9408241-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contain start or stop codons'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_except= pos:622..624,aa:Arg
/note= "partial CDS, therefore sequence does not
                                                                                                      WO9408241-A.
                                                                                                                   contain start or stop codons'
                                                                                                                                 /transl_except= pos:700..702,aa:Arg
/note= **partial CDS, therefore sequence
                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                       anti-oncogene;
                                                                                                                                                                                                                                                                     Fragment coding for human p53 amino acids 40-393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; R51876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-oncogene; cancer; tumour; antibody binding region; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragment coding for human p53 amino acids 66-393.
                                                                                                                                                             /product= p53(40-393)
                                                                                                                                                                                                                                                                                   18-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= p53(66-393)
                                                                                     14-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                       842 aggccttggaactcaaggatgcccaggct 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE-232823.
                                                                                                                                                                                                                                                       phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                       cancer; tumour; antibody binding region; epitope;
                                                                                                                                                                                             Location/Qualifiers 1..1062
                                                                                                                                                                                                                                                                                                                 cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 11;
Pred. No. 2.07e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volkmann M,
                                                                                                                                    does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 984;
                             Zentgraf
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Best Local Similarity 82.8%;
Matches 24; Conservative
                                                              Matches
                                                                         Query Match 50.0%;
Best Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                       04-JAN-1994; US-176937.
23-MAY-1994; US-247904.
27-MAY-1994; US-250795.
13-SEP-1994; US-305520.
                              1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q97854;
                                                                                                                                                 Disclosure; Page 105-106; 157pp; English. Human p53 cDNA (given in Q97854) was amplified from a HeLa ce. CDNA library using the primers given in Q97852-53. The gene was subcloned into a baculovirus vector for expression of recombinant p53 in Sf9 insect cells for use as a component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ubiquitin-conjugating enzyme; p53 protein; cell cycle; cell proliferation; cancer; psoriasis; fibrosis; ds.
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Q97854 standard; cDNA; 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-radioactive detection of p53 specific antibodies - by on immobilised p53 or its fragments, then reaction with lasecond antibody, for diagnosis of tumours and suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 22; 35pp; German.
                                                                                                                    an in vitro ubiquitin conjugating system. Sequence 1181 BP; 275 A; 366 C;
                                                                                                                                                                                                                               e.g. cell proliferation
                                                                                                                                                                                                                                                          regulatory proteins - also new ubiquitin conjugating enzymes, their
                                                                                                                                                                                                                                                                                             P-PSDB; R79658.
                                                                                                                                                                                                                                                                                                          WPI; 95-255137/33.
                                                                                                                                                                                                                                                                                                                        Cottarel G,
                                                                                                                                                                                                                                                                                                                                        (MITO-) MITOTIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human p53 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            each of these fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368-386. See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies specific for p53 are detected by binding to immobilised fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening
                                                                                                                                                                                                                                           related nucleic acid, vectors, antibodies etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                          dentifying inhibitors of ubiquitin mediated proteolysis of cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                   L3-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     920 aggeettggaactcaaggatgeecagget 948
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AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
               aggccttggaactcaaggatgcccaggct 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1062 BP;
                                                                                                                                                                                                                                                                                                                        Draetta G,
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 A;
                                                                                                                                                                                                                                                                                                                        Eckstein JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 11;
Pred. No. 2.07e-01;
                                                                         Score 19; DB 15;
Pred. No. 2.07e-01;
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                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                        Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 G;
                                                                                                                      306 G;
                                                           5.
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                                                                                         Length 1181;
                                                                                                                                                                                                                                               useful for regulating
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                                                                                                                                                                                                 a HeLa cell
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                                                                                                                       234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by capture
                                                                                                                                                                                                                                                                                                                        33
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Best Local S
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          18-MAR-1992.
23-AUG-1991; 307791.
24-AUG-1990; US-573405.
(REGC) UNIV OF CALIFORNIA.
Lee WH, Chen PL;
WPI; 92-090221/12.
                                                                                                                                                                                                                                                        Use of wild-type p53 gene - in a medicament for suppressing the neoplastic phenotype of a cancer cell lacking wild-type p53 protein Claim 1; Page 5; 25pp; English.

The wild-type p53 gene can be used in the production of a medicament for suppressing the neoplastic phenotype of a cancer cell lacking
                                                                                                                                                  23-JUL-1992 (first entry)
Sequence encoding 53 kD cellular protein.
Cancer therapy; cancer suppressor gene; o
                                                                                      EP-475623-A.
                                                                                                                                       Homo sapiens.
                                                                                                                                                                                          Q22995;
                                                                                                                                                                                                      Q22995 standard; DNA; 1182 BP
                                                                                                                                                                                                                                                                                                  50.0%; t Local Similarity 82.8%; it ches 24; Conservation
                                                                                                                                                                                                                                                                                                                                                                         or prostate carcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                     endogenous ward type por process. Jung carcinoma cells, lymphoma fashion include osteosarcoma cells, lung carcinoma cells or breast, bladder
                                                                                                                                                                                                                                                                                                                                                                                                             endogenous wild type p53 protein. Cancer cells suppressed in such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= p53 protein.
misc_difference 19..21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p53 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 96-223439/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= CAT encodes
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                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia cells; soft tissue sarcoma cells; breast cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; carcinoma; neoplastic; neoplasia;
                                                                                                                                                                                                                                                                                                                                                               1182 BP;
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                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             278 A;
                                                                                                                                                                                                                                                                                                                      Score 19; DB 22;
Pred. No. 2.07e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspartic
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                                                                                                                                                                                                                                                                                                                                                             366 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid.
                                                                                                                                                      oncogenesis;
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                                                                                                                                                                                                                                                                                                                                                             234 T;
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Best Local Similarity 82.8%;
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1037 aggccttggaactcaaggatgcccaggct 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; murine; interleukin-2; IL-2; pNR825; pmut-1; pBS-SK; pMM151; TK vector plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; polymerase chain reaction; poxvirus; pSD542; immunological response; pathogen; human; interferon; IFN; ss.
                                                                                                                                                                                                 virus produced recombinant virus vCP270, which contains the vaccinia H6 promoted mutated human p53 in the C5 locus. The resulting virus may be
                                                                                                                                                                                                                                      position 524, changing an Arg residue at position 175 to a His residue. The plasmid pMMIIO (see also 067884) contains the vaccinia H6 promoter and the wild type human p53 gene in the ALVAC C5 insertion site. The mutant p53 gene was obtained from plasmid Cx22A and cloned into pMMIIO to generate pMMI43. Recombination between pMMI43 and ALVAC rescuing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1182 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon carcinoma, lymphoma, leukaemia, etc., suggesting that mutation of the pS3 genes is involved in oncogenesis. Specifically 273 Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes. Variant forms of p53 are found in human breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p53 cDNA, or its gene prods., can be used to suppress and eradicate cancers caused by defective, mutant or absent cancer suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is replaced by 273 His, a mutation found exclusively in tumour cells. Sequence 1182 BP; 277 A; 368 C; 303 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 15; 25pp; English.
                                                                                                                                          Sequence
                                                                                                                                                                              used in a composition for inducing an antigenic or immunological
                                                                                                                                                                                                                                                                                                                                                                construction of an ALVAC-based recombinant virus containing a mutant
                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the wildtype human p53 gene from the translation
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 32; Fig 39; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cytokine and/or tumour associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 94-263767/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VIRO-) VIROGENETICS CORP.

Cox WI, Paoletti E, Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1994; U00888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09416716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human p53 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q67884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q67884 standard; DNA; 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neoplastic phenotype e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloned p53 cDNA and protein prods. - for suppression of
                                                                                                                                                                                                                                                                                                                                           form of the human p53 gene. The mutant form has a G>A substitution at
                                                                                                                                                                                                                                                                                                                                                                                   initiation codon to the stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ymphoma(s), etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 50.0%;
Local Similarity 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                           24;
                                                                                                                                          1182 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                           Conservative
                                                                                                                                                           for immunisation against pathogens.
                                                                                                                                        276 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.07e-01;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  쁑
                                                                         Score 19; DB 12;
Pred. No. 2.07e-01

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteo-sarcuma(s), leukaemia(s)
                                                                                                                                        365 C;
                                                                                                                                                                                                                                                                                                                                                                               This sequence was used in the
                                                                                                                                        307 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1182;
                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç.
                                                                                               Length 1182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                           Indels
                                                                                                                                        234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung or
                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TK vector;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                           0
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5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33

Ş Matches Query Match 50.0%; Best Local Similarity 82.8%; 1269 aggccttggaactcaaggatgcccaggct 1297 viruses, and into NYVAC to give vP1101, vP1096 and vP1098. The viruses may be used in a composition for inducing an antigenic immunological response, ie. for immunisation against pathogens. Sequence 1483 BP; 367 A; 415 C; 372 G; 329 T; mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI and p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53 Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53wtXbaISP6/T3; p53-21XbaI; p53-238XbaI; vaccinia; H6 promoter; plasmid; pRW825; expression cassette; Q67864; plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant gene. The expression cassettes generated by linking the vaccinia H6 promoter and the p53 genes may be cloned in to the poxvirus insertion construction of poxvirus based recombinant viruses expressing wild type and mutant forms of the human p53 gene product. The wild type and containing the vaccinia H6 promoter and the wild type human p53 gene in vP1101 and vCP207, respectively. These sequences were used in the DNA encoding cytokine and/or tumour associated antigen Example 15; Fig 18; 232pp; English.

The sequences given in 06/863-64 represent expression cassettes WPI; 94-263767/32. Cox WI, ALVAC (CPpp) p53; poxvirus; antigenic response; immunological response; Vaccinia H6 promoter/human p53 expression cassette from vCP207. Q67864 standard; Attenuated recombinant virus used for cancer therapy - comprises 19-JAN-1994; US-184009 21-JAN-1993; 04-AUG-1994. WO9416716-A. /note= "Flanking sequence" misc feature promoter misc feature Synthetic. pathogen; ss. 22-MAR-1995 (VIRO-) VIROGENETICS CORP. 21-JAN-1994; U00888 /product= Wild type human /note= "Vaccinia H6 promoter" CDS 233..1414 /\*tag= c note= "Flanking" Paoletti E, Tartaglia J; (first entry) us-007115. Conservative g sequence"
109..232 Location/Qualifiers 1..108 1415..1483 DNA; 1483 BP Score 19; DB 12; Pred. No. 2.07e-01; 0; Mismatches 5. Length 1483; 0; These nic or Gaps the <u>.</u>.

267863; Q67863 standard;

DNA;

1512 ВP

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RESULT
ID Q2
AC Q2
DT 11
DE Mu
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Best Local Similarity 82.8%;
                                                                                                                                                                                                                                            1305 aggccttggaactcaaggatgcccaggct 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construction of poxvirus based recombinant viruses expressing wild type and mutant forms of the human p53 gene product. The wild type and mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI and p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5-most region of the p53 product of the p54 product o
                                                        UT 14
Q27944 standard; cDNA; 1740 BP
Q27944;
Mutant p53 polypeptide (Hup53HIS273).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter and the p53 genes may be cloned in to the poxvirus insertion plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cox WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses, and into NYVAC to give vP1101, vP1096 and vP1098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          containing the vaccinia H6 promoter and the wild type human p53 gene in vP1101 and vCP207, respectively. These sequences were used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
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                            11-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viruses may be used in a composition for inducing an antigenic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in Q67863-64 represent expression cassettes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Fig 17; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding cytokine and/or tumour associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Attenuated recombinant virus used for cancer therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 94-263767/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-1994; U00888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9416716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Vaccinia H6 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*cag= a
/note= *Flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALVAC(CPpp)p53; poxvirus; antigenic response; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccinia H6 promoter/human p53 expression cassette from vP1101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunological response, ie. for immunisation against pathogens. sequence 1512 BP; 379 A; 419 C; 380 G; 334 \mathrm{T}_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ′*tag= c
                                                                                                                                                                                                                  5 AGGCCTTAGAGTTAAAGGATGCCCATGCT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The expression cassettes generated by linking the vaccinia H6
                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paoletti E, Tartaglia J;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wildtype p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145..268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269..1450
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.07e-01
                                                                                                                                                                                                                                                                                                                                                                                                   Score 19;
                                                                                                                                                                                                                                                                                                                                    <u>,</u>.
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 1512;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises
                                                                                                                                                                                                                                                                                                                                       0
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Best Local Similarity 82.8%;
Matches 24; Conservative
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Q51787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1992;
31-JAN-1992;
01-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1325 aggccttggaactcaaggatgcccaggct 1353
/rpt_type= tandem /rnote= "can be repeated z times, where z is 1-4, provided that y+z is 6-12; N stands for identical or different nucleotides, excluding stop codons" us5227293-A.
                                                                                                                                                                                                                                                                                                                         /rpt type= tandem
/rpt type= tandem
/note= "can be repeated y times, where y is 4-11,
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21-JUN-1991; US-719172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mixed oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; ballast constituent; pro-insulin production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mixed oligonucleotide #19 encodes ballast constituent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence derived from activated p53 oncogene given in the specification has been published by Harlow E. et al. (1985) Molecular and Cellular Biology 5:1601-1610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library was constructed using mRNA extracted from A431 cells (express Hup53HIS273) as described by Harlow E. et al., (1985) J. Virol. 37:1601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present intracellularly at high concns. in mammalian tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant p53 polypeptides encoded by activated p53 oncogenes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 52; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              presence of mutant p53 polypeptide in a fluid sample from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing a neoplastic condition in a subject -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 92-300054/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uncogene; tumour; neopiasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant protein production; HMG CoA reductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and expression of mutant p53 polypeptide is described, where a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide conc. and the presence of neoplastic disease provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sub ject
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ONCO-) ONCOGENE SCI INC.
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                                                                                                                                                                                                                                                                                            /note= "(DCD)11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The correlation between the measured mutant p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.07e-01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1740
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PP 13-JUL-1993.

PF 29-AUG-1989; 399874.

PR 29-AUG-1989; US-399874.

PR 29-AUG-1989; US-399874.

PR 23-APR-1992; US-382221.

PA (EEHO) GEN MOSPITAL CORP.

PA (EEHO) J GEN MOSPITAL CORP.

PA (FARH) HOECHST AG.

PI Habermann P, Seed B, Stengelin S, Uhlmann E, Ulmer W;

PWP1; 93-235119/79.

PT Fusion proteins for prodn. of e.g. pro-insulin - comprise gene

PT for desired protein and oligo-nucleotide(s) encoding ballast

PS Claim 9; Column 30; 22pp; English.

CC This preferred mixed oligonucleotide encodes a ballast constituent

CC and is inserted between a regulatory region and the structural gene

CC component improves protease resistance of the fusion protein while

CC still allowing the desired protein to adopt its correct conformation

CC prior to cleavage of the ballast constituent.

SQ Sequence 39 BP; 1 A; 11 C; 1 G; 1 T;

Query Match

47.4%; Score 18; DB 7; Length 39;

Best Local Similarity 18.8%; Pred. No. 7.47e-01;

Matches 6; Conservative 19; Mismatches 7; Indels 0; Gaps 0;

PS Search completed: Tue Mar 25 02:42:45 1997

Job time: 15 secs.
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Mar 24 II:15 US-08-644-289-1 rag

Mar 24 11:15

US-08-644-289-1\_rag

(i)

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 24 11:17:33 1997; MasPar time 1.84 Seconds 111.735 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-1
Description: (1-20) from US08644289.pep
Perfect Score: 151
Sequence: 1 SLRPFKALVREKGHRPSHSC 20

Scoring table: PAM 150 Gap 15

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 20.568; Variance 59.693; scale 0.345

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Match Length DB		ID	Description	Pred. No.
_	151	100.0	- 1	18	R92698	Human wild-type p53 q	8.31e-11
2	60	39.7		w	R13252	Murine Cytotoxic Cell	1.53e+01
ω	60	39.7		G	R27651	Human calcium channel	
4	60	39.7		ഗ	R27650	Human calcium channel	
5	60	39.7		ü	R73055	Rabbit skeletal calci	
6	60	39.7	1873	<u></u>	P95645	Rabbit seletal muscle	
7	60	39.7	1967	6	R33547	Sequence of the alpha	
<b>&amp;</b>	69	39.7	2138	14	R72607	Human neuronal calciu	1.53e+01
9	60	39.7	2161	14	R71002	Human neuronal calciu	
10	60	39.7	2161	14	R71001	Human neuronal calciu	
11	60	39.7	2161	δ	R33545	Sequence of the alpha	
12	60	39.7	2163	14	R71003	Human neuronal calciu	1.53e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
51	51	51	51	51	51	52	52	52	52	53	53	53	53	53	53	53	53	53	53	53	53	54	54	54	54	54	54	54	55	57	57	57
•	•	•	•		33.8	•	34.4	34.4	34.4	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.1	35.8	•	•	•		35.8	35.8	36.4	37.7	37.7	37.7
1196	567	385	305	118	118	690	436	436	223	2020	2019	1989	1989	1984	1977	1835	1693	1011	399	148	99	2813	2813	885	677	256	256	237	685	3164	553	349
16	18	14	17	13	12	ω	17	17	7					18				18	7		13				_		15	4		_		
R75189	R87531	R76578	R89750	R74338	R67373	R15482	R98146	R98143	R37573	R06584	R67913	R92317	R99640	R99639	R99641	R92316	R51264	R99638	R33934	R29180	R72089	P60462	P60053	R92747	R95692	R45403	R85639	R20509	R11331	R94346	R13944	R20784
Osteoinductive retrov	S	Coriander omega-12 de	AFT-1 (Arabidopsis fo	Helicobacter pylori h	Heat shock protein HS	Protein encoded by OR	Tne DNA polymerase N-	Tne DNA polymerase.	Partial human skeleta		dium chan	nervous	nervous	nervous	nervous	nervous	protein	l ner	Morphogen mOP2 full 1	rovir	region.	of.	er.	SA8 virus qB qlycopro	holine acetyl	വ	preproPR-3.	Human proteinase 3.	ب		al HVT ribo	Tulip allylacyl amida
1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.07e+02	1.07e+02	1.07e+02	1.07e+02					8.43e+01	8.43e+01		8.43e+01		٠						•	•	•	6.64e+01	٠.		٠.	3.21e+0

# ALI GNMENTS

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Sequence

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Matches Query Match

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y Match 100.0%; Local Similarity 100.0%;

Score 151; DB 18; Pred. No. 8.31e-11;

Length Indels

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23-MAR-1992; 104970.
04-APR-1991; DE-110785.
(FARB ) BAYER AG.
Franz J, Rae P, Unterbeck A, Weingaertner
                                                                                                                                                                                                                                                                                                                                           R27651 standard; Protein; 619 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein was used to design peptides which competitively inhibit the protease. See also Q12863-6 and R13254-R13262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bleackley RC, Lobe CG, Paetkau VH, James MN, Murphy M; WPI; 91-237989/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine Cytotoxic Cell Protease-1.
mouse; CCP-1 inhibitor; cytotoxic T-lymphocytes; ss.
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                                                                                                                              07-OCT-1992.
                                                                                                                                                              EP-507170-A.
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                         Plasmid pCA9.3; Ca-flux assay.
                                                                                                                                                                                                                                                         Human calcium channel 27980/13.
                                                                                                                                                                                                                                                                                    03-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                       R27651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of CCP-1 was predicted from the cDNA sequence. The structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The CCP-1 coding sequence was isolated from the cytotoxic T-cell line MTL 2.8.2 generated from CBA/J mice. The amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA vectors, and inhibitors of cytotoxic cell protease - f treatment of auto-immune diseases e.g. pernicious anaemia, rheumatoid arthritis, allo-graft rejection etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R13252 standard; Protein; 247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JAN-1990; US-467880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1991; U00340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 rpymallsikdqqpeaic 49
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ilarity 38.9%;
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Pred. No. 1.53e+01;
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RESULTION ACCORDANCE FOR MANAGEMENT AND ACCORDANCE FOR ACCORDANCE 
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                              Query Match 39.7%;
Best Local Similarity 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
   Matches
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                                                                                                                                                            and IV and part of the C-terminus coding sequence. The human neuronal calcium channel protein can be used for screening for Cachannel ligands (agonists or antagonists). See also Q29259-Q29275
                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium flux assays to screen for neurone-specific calcium channel ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Franz J, Rae P, Unterbeck A, Weingaertner B; WPI; 92-333446/41.
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloned human neuronal calcium channel sub-types - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q29270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1992; 104970
04-APR-1991; DE-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pCA3; Ca-flux assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human calcium channel 27980/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R27650 standard; Protein; 993 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuronal calcium channel protein can be used for screening for Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 83-85; 101pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channel ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium flux assays to screen for neurone-specific calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloned human neuronal calcium channel sub-types - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q29271.
                                                                                                                                                                                                                                                           Domains II and III. The clone comprises the complete Domains III
                                                                                                                                                                                                                                                                                                                              containing carp skeletal muscle Ca-channel cDNA. The cDNA clone
                                                                                                                                                                                                                                                                                                                                                                cortex and visual cortex cDNA banks were screened with a probe
                                                                                                                                                                                                                                                                                                                                                                                               Human neuroblastoma cell line, hippocampus, frontal and temporal
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 78-82; 101pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP-507170-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channel ligands (agonists or antagonists). See also Q29259-Q29275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 92-333446/41.
                                                                                                                                                                                                                                                                                          pCA3 was sequenced. The 5'end of the clone lies between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-0CT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "corresponds to nonsense codon TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "corresponds to nonsense codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 lrplrainrakglkhvvqc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 39.7%;
Local Similarity 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LRPFKALVREKGHRPSHSC
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                                                                                                                                   993 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE-110785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 5; Lengt; Pred. No. 1.53e+01; No. 1.53e+01;
                                 Score 60; DB 5; I
Pred. No. 1.53e+01;
   4;
   Mismatches
                                                                Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 619;
   7:
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   Gaps
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RESULT

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ACC DE COL
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| Modified site 191
| Modified site 191
| Modified site 1464
                                         Region 433
/label= see above
Region 467
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                                                                                                                                  Region 199
/label= see above
Region 310
/label= see above
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/label= see above
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1552
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/label= see above
1757 gite 1757
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Misc_difference 1835
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R73055;
02-NOV-1995 (first entry)
Rabbit skeletal calcium channel (alpha)1-subunit.
Calcium channel; (alpha)1 subunit.
Region 4
/label= see above
                                                                                                                                                                                                                                                                            Region 12
/label= see above
                                                                                                                                                                                                                                                                                  rotein
/label= see above
121..139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= potential cAMP-dependent phosporylation Modified site 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "In Tanabe et al"
Misc_difference 1815
                                                                                                                                                                                                                                Region 10
/label= see above
                                                                                                                                                                                                                                                                                                                                             /label= transmembrane region
Protein 89..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= see above
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Ala
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ed site 1854
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                                                                 467..486
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                       495..513
                                                                                                                 433..451
                                                                                                                                                               310..334
                                                                                                                                                                                                        199..218
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902 lrplrainrakglkhvvqc 920

Query Match 39.7%; Best Local Similarity 42.1%; Matches 8; Conservative

Score 60; DB 13; Length 1873; Pred. No. 1.53e+01; 4; Mismatches 7; Indels 0;

Gaps

0

Ower Match		in K/3055	consisting	cDNA is cl	CC transmembrane segments.					deduced AA	three (see	318, 1987.		receptor		PS Disclosure: Fig 1: 32pp	[me.]	FOY				SALL	13-JUL-1992;	04-APR-1989;	04-APR-1988;		US5407820-A.	= see	Region	= see	Region see	Kegion	= see	Region	/label= see	Region	/label= see	Region	regron	/label= see	Region	/label= see	Region	/label= see	FT Region	(1abol- aco	= See	Region	/label= see	Region	FT /label= see a	
20 74. Garage CO. PD 12. Targeth 1072.	18/3 AA;	ith the Tanabe et	that encodes a protein that has the AA seque		A eukaryotic cell expressing a chi	sequence regions. It has been proposed	that described by Tanabe et al. It contains four	phoresis. The AA sequence is 99.8%	using SDS	a calculated Mr of 212, 143, in	A changes (see R73055 FT)	ferences were identified at 33 posns, of whi	receptor reported by Tanabe	mRNA. It is 94% identical to the cond segment	087978 is consistent with an	3300.	restricting caretima chainser agontocovanicagonitses of		1 1 1 1 1 1 1 1	88/21.	Ellis SB, Harpoid MM, Schwartz A, Williams ME;	BIOTECHNOLOGY IND ASSOC.	US-914231.	US-603751.	US-176899.	176899.		above	12701289	above	above 1939 1950	11811199		11531172		11191137	above	1041 . 1065	301300	above	, 893912	above	867885	above	835_854	000010	above gnn gng	637661	above	562581	above	- 33

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2 LRPFKALVREKGHRPSHSC

P95645 standard;

protein; 1873

A

P95645

04-APR-1988; 001408. 04-APR-1988; US-176899. (SALK) Salk Inst for Biol Stud.

W08909834-A.

19-OCT-1989.

Sylvilagus (rabbit). Skeletal muscle Rabbit seletal muscle alpha-1 sub-unit gene product.

21-MAR-1990 (first entry)

Ellis SB, Williams ME, Harpold MM, Schwartz A, Sartor J; WPI; 89-324236/44.

N-PSDB; N91778.

New DNA encoding alpha-2 subunit of animal calcium channel - also new

protein product and eukaryotic cells for testing cpds. for calcium

agonist or antagonist activity

Disclosure; page 16-1 to 18-3; 68pp; English. Also used to diagnose Lambert-Eaton syndrome by reacting test serum with alpha-1 and alpha-2 subunits. Labelled fragments can be used as

probes.

Sequence

1873 AA;

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SS CC

Sequence

1967 AA;

encodes an alternative exon

for the IV S3 transmembrane domain

US-08-644-289-11rag

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RESULT
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                                      Numerous alpha IC-specific DNA clones were isolated. Characterisation of the sequence revealed the alpha IC coding sequence, the alpha IC initiation of translation sequenc, and an alternatively spliced region of alpha IC. Q37814 and Q37815 encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-1992; U06903.
15-AUG-1991; US-745206.
10-APR-1992; US-868354.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                DNA encoding specific human calcium channel sub-units - used for
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 93-093936/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brenner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R33547;
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                                                                                                                                                                                                        Disclosure; Page 102-109; 150pp; English.
                                                                                                                                                                                                                                                   diagnosing Lambert Eaton syndrome
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q37813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         м09304083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lambert Eaton syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human calcium channel subunit; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the alpha 1C human calcium channel subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                             identifying calcium channel agonists and antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               902 lrplrainrakglkhvvqc 920
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possible amino terminal ends of the alpha 1C protein. Q37816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRPFKALVREKGHRPSHSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feldman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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Pred. No. 1.53e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Calcium channel subunit; antagonist; agonist; diagnosis;

RESULT
ACCOMENTATION
PRINTED
P RESULT Š 밁 Ş 밁 Best Matches Query Match 39.7%; Best Local Similarity 42.1%; Matches Query Match 1003 lrplrainrakglkhvvqc 1021 translation and an alternatively spliced region. Q84655 sets forth one alpha 1c coding sequence (alpha 1c-1) and R71003 sets out its deduced AA sequence. Q87834 and R72607 set out another obtaining agonists and antagonists Claim 34; Page 260-269; 285pp; English. Numerous alpha 1c-specific cDNA clones were isolated in order to 05-NOV-1993; US-149097. (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. (Ellis SB, Gillespie A, Harpold MM, Mccue T 8 R72607 standard; Protein; 2138 Human neuronal calcium channel subunit alpha 1D including exon encoding the 1S6 transmembrane domain. R71002 standard; Protein; 2161 R71002; and/or inserting the alternative exon in the appropriate location (see Q84655 FT). In addition, a nt. sequence (see Q84655 alpha ic variants can be constructed by selecting alternative amino terminal ends in place of the ends in Q84655 and Q87834 splice variant, designated alpha 1c-2. Q84656 encodes an Human neuronal calcium channel subunit alpha 1c-2. Calcium channel subunit; antagonist; agonist; diagnosis; 01-DEC-1995 (first entry) R72607; 1027 lrplrainrakglkhvvqc 1045 Sequence alternative exon for the IV S3 transmembrane domain. Other characterise the alpha 1c coding sequence, the initiation developing prods. for studying calcium channels, e.g. N-PSDB; Q87834. WPI; 95-090900/12. Homo sapiens. 30-NOV-1995 (first entry) splice variant. FT) can be deleted or inserted to produce an alternative alpha DNA encoding human calcium channel sub-unit(s) - used WO9504822-A. Lambert Eaton Syndrome. 11-AUG-1993; US-105536. l1-AUG-1994; U09230. 6-FEB-1995. Match 39.7%; Local Similarity 42.1%; 2 LRPFKALVREKGHRPSHSC 2 LRPFKALVREKGHRPSHSC = ::: = :: = = = = <u>«</u> 8 2138 AA; Conservative Conservative 20 Score 60; DB 14; Leno, Pred. No. 1.53e+01; "'Amatches 7; Pred. Score 4; A A Mismatches 60; DB 6; I No. 1.53e+01; Æ, Length 1967 Length 2138; Williams ME; Indels <u>.</u> 0, Gaps Gaps <u>.</u> 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human alpha 1D subunit was obtd. Full-length clones were then constructed by ligating partial clones. Q84653 shows the nt sequence of the CDNA encoding the alpha 1D subunit. The Albha 1D protein has a calculated Mr of 245,163. It contains four putative internal repeated sequence regions which represent 24 putative transmembrane segments. It mediates DHP-sensitive high-voltage, long-lasting
                                                                                                 (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. Ellis SB, Gillespie A, Harpold MM, Mccu WPI; 95-090900/12.
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
W09504822-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R71001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium channel activity. Q84654 shows an alternative exon encoding the IS6 transmembrane domain. The difference occurs in AAs 373-
DNA encoding human calcium channel sub-unit(s) - developing prods. for studying calcium channels,
                                                                                                                                                                                               11-AUG-1993; US-105536.
05-NOV-1993; US-149097.
                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human neuronal calcium channel subunit alpha 1D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R71001 standard; Protein; 2161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe to screen a cDNA library of human neuroblastoma cell line IMM32, to obtain clone alphal.36, This close was used as a probe to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The alpha 1D subunit cDNA has been isolated using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obtaining agonists and antagonists Disclosure; Page 126-127; 285pp; Er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1993; US-149097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9504822-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key Location/Qualifiers Misc_difference 373..406
                                                                      N-PSDB; Q84653.
                                                                                                                                                                                                                                                               11-AUG-1994; U09230.
                                                                                                                                                                                                                                                                                              16-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                               Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 series of clones to span the length of the nt seuence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clones, which were then employed for screening until a sufficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scren additional IMR32 cell cDNa libraries to obtain overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing prods. for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human calcium channel sub-unit(s) - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q84654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1993; US-105536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1994; U09230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= encoded by alternative exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lambert Eaton Syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        989 lrplrainrakglkhvvqc 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 39.7%;
Local Similarity 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRPFKALVREKGHRPSHSC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pha 1D subunit cDNA has been isolated using fragments of the skeletal muscle calcium channel alpha 1 subunit cDNA as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gillespie A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 14; Pred. No. 1.53e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccue AF,
                                                                                                                               Мссце
-unit(s) - used channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 2161;
                                                                                                                               Æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams ME;
                                                                                                                                   Williams
                                                                                                                               Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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obtaining agonists and antagonists

US-08-644-289-1\_rag

RESULTATION AND ACCORDANCE OF PART OF 맑 Ş Matches Query Match 39.7%; Best Local Similarity 42.1%; Query Match rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a probe to screen a cDNA library of human neuroblastoma cell line IMR32, to obtain clone alphal.36, This close was used as a probe to screen additional IMR32 cell cDNA libraries to obtain overlapping clones, which were then employed for screening until a sufficient series of clones to span the length of the nt seuence encoding the The alpha 1D subunit cDNA was isolated using fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit cDNA as a probe to screen a cDNA library of a human neuroblastoma cell line, IMR32, to obtain clone alpha 1.36. This clone was used as a probe to screen additional IMR32 cell cDNA libraries to obtain overlapping R33545 standard; Protein; 2161 constructed by ligating partial clones. Q84653 shows the nt sequence of the cDNA encoding the alpha 1D subunit. The Alpha 1D protein has Sequence transmembrane domain of the alpha 1D subunit. The alpha 1D protein has a calculated Mr of 245,163. encoding the human alpha 1D subunit were obtained, see Q37811. clones which were then employed for screening until a sufficient series of clones to span the length of the nucleotide sequence Brenner R, Homo sapiens. Human calcium channel subunit; diagnosis; agonist; antagonist; Sequence of the alpha 1D human calcium channel subunit. R33545 Sequence calcium channel activity. a calculated Mr of 245,163. It contains four putative internal Q37812 provides the sequence of an alternative exon encoding the IS6diagnosing Lambert Eaton syndrome Disclosure; Page 93-101; 150pp; English. N-PSDB; Q37811. Williams ME; 04-MAR-1993. WO9304083-A. segments. It mediates DHP-sensitive high-voltage, long-lasting repeated sequence regions which represent 24 putative transmembrane human alpha 1D subunit was obtd. Full-length clones were then DNA encoding specific human calcium channel sub-units - used WPI; 93-093936/11. (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. Brenner R, Ellis SB, Feldman DH, Harpol 10-APR-1992; US-868354. 15-AUG-1991; US-745206. 14-AUG-1992; U06903 Lambert Eaton syndrome. 30-JUN-1993 The alpha 1D subunit cDNA has been isolated using fragments of the Disclosure; Page 116-126; dentifying calcium channel agonists and antagonists and 989 lrplrainrakglkhvvqc 1007 2 LRPFKALVREKGHRPSHSC 20 œ --2161 AA; 2161 AA; Conservative (first entry) 39.7%; 42.1%; 285pp; English. Score Pred. Score 60; DB 14; Pred. No. 1.53e+01; AA. Mismatches No. Harpold MM, DB 6; Length 2161; Length 2161; Mccue Indels Æ 0; for Gaps 0

Best Local Similarity

1.53e+01;

Matches

**8** 

Conservative

4:

Mismatches 7; Indels

<u>.</u>

Gaps

<u>,</u>

Mar 24 11:15

US-08-644-289-1\_rag

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RESULT
ID R2
AC R2
DT 12
DE Tu
KW Ch
OS Tu
PN J0
PD 19
PF 06
PR 06
PA (N
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                                                                                                                                                                                                                                                                                          Query Match
39.7%;
Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-AUG-1994; VV-1-1
11-AUG-1993; US-105536.
05-NOV-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  obtaining agonists and antagonists
Disclosure; Page 127-137; 285pp; English.
Numerous alpha 1c-specific cDNA clones were isolated in order to characterise the alpha 1c coding sequence, the initiation of translation and an alternatively spliced region. Q84655 sets forth one alpha 1c coding sequence (alpha 1c-1) and R71003 sets out its deduced AA sequence. Q87834 and R72607 set out another
               Chemical selection; herbicide resistance. Tulippa. J03290190-A. 19-DEC-1991. 06-APR-1990; 091565. 06-APR-1990; JP-091565.
                                                                                                                                                             R20784 standard; Protein; 349 AA.
                                                                                                                                                                                                                                                             1028 lrplrainrakglkhvvqc 1046
                                                                                                                                                                                                                                                                                                                                                                                          and/or inserting the alternative exon in the appropriate location (see Q84655 FT). In addition, a nt. requence (see Q84655 FT) can be deleted or inserted to produce an alternative alpha lo
                                                                                                               Tulip allylacyl amidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ellis SB, Gillesp. WPI; 95-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R71003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R71003 standard; Protein; 2163 AA.
                                                                                                                                                  R20784;
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                              splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                            amino terminal ends in place of the ends in Q84655 and Q87834
                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha lc variants can be constructed by selecting alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative exon for the IV S3 transmembrane domain. Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           splice variant, designated alpha 1c-2. Q84656 encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developing prods. for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding human calcium channel sub-unit(s) - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q84655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
WO9504822-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human neuronal calcium channel subunit alpha 1c-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1995 (first entry)
                                                                                                                                12-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lambert Eaton Syndrome.
   (NORQ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l6-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       989 lrplrainrakglkhvvqc 1007
                                                                                                                                                                                                                              2 LRPFKALVREKGHRPSHSC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LRPFKALVREKGHRPSHSC 20
   NORINSHO.
                                                                                                                                                                                                                                                                                                                                                             2163 AA;
                                                                                                                                                                                                                                                                                                              Score 60; DB 14; Length 2163; Pred. No. 1.53e+01;
                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mccue AF,
                                                                                                                                                                                                                                                                                             7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                                                                                                                                                           Gaps
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В Q

415 lrpysqlird 424 |||: |:|: 2 LRPFKALVRE 11

3		
₩ ₩	WPI; 92-045622/06. N-PSDB: 020497.	
i	DNA encoding tulip allacyl amidase - useful in chemical selection and	
Š	prodn. of nerbicide resistant plants. Disclosure; Fig 3; 11pp; Japanese.	
ದ ದ	Crude allylacyl amidase was prepd. from tulip bulbs and purified by dialysis. DEAE cellulose chromatography, gel filtration and	
; K	hydroxyapatite chromatography. The purified protein was partially	
K K	digested by Lysyl endopeptidase and the protein fragment sept. by SDS-PAGE. The amino acid sequence was determined and the crude	
888	ein used to prepare rabbit ant en a cDNA library, constructed	
8 8	poly $\mathtt{A}$ + RNA. The base sequence and corresp. amino acid sequence were then determined.	
ŏ	Sequence 349 AA;	
9	Query Match 37.7%; Score 57; DB 4; Length 349;	
Ma		
8	tvkp	
y	6 KALVREKGHRPSHSC 20	
RESULT	JT 14	
5 E	R13944 standard; Protein; 553 AA.	
ĭ	27-NOV-1991 (first entry)	
<b>£</b> 6	re	
žŏ	126.	
ĕ	18-SEP-1991.	
ž ř	U)-MAR-1991; 400534. 12-MAR-1990: FR-003105.	
Ä	M	
Ħ ĭ	Rey-Senelonge A, Kohen G; WPI: 91-275886/38	
Ħ		
řř	New herpes recombinants - useful as vaccines against human and animal viral conditions, e.g. fowl pest, coccidiosis and	
ĭ		
လိုက်	Disclosure; Page 13-14; 22pp; French. This sequence is the C-terminal region of HVT RR1. It was deduced	
i ii	m a genomic DNA clone which	
පි පි	the entire RRZ gene. Knowledge of the RRZ small sub-unit sequence is exploited in the construction of recombinant vaccines. A heterologous	
i ii	sequence coding for an appropriate immunogen to protect against e.g.	
S S	bronchitis, etc. is inserted into the RR2 gene. The HVT is suitable	
ಗ ಗ	for use in live vaccines as it is apathogenic and non-oncogenic. See also 013668.	
ö	Sequence 553 AA;	
ng G	37.7%; Score 57;	
Ma.	Similarity 50.0%; Pred. No. 3.21e+01; 5: Conservative 3: Mismatches 2: Inc	
	C. CHECK PARTY C. TENNISH C. TIME C.	

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S
                                   밁
                                                                 Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1995.

14-FEB-1995; U02118.

14-FEB-1994; US-196030.

13-MAY-1994; US-242654.

29-JUL-1994; US-283314.

23-NOV-1994; US-344190.

23-NOV-1994; US-344185.
                                   1980 rrrgyrprhac 1990
                                                                                                                                                         infected tamarin plasma, using standard procedures, was used to prepare a lambda phage HGBV cDNA library. Clones were rescued from the lambda phage, searched against a sequence database and found to be unique HGBV sequences. The clones were then used to assemble the sequences T00129/30 (GB contig A and B) which encode the proteins R9435-47 (the 3 possible coding strand reading frames) and R82072, respectively. Reagents which comprise the HGBV DNA, or its protein prods. can be used for the diagnosis, therapy or in a vaccine to prevent HGBV infection.
                                                                                                                                                                                                                                                                                                                   N-PSDB; T00129.

Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful for diagnosis and therapy of hepatitis GB virus Example 9; Pages 343-357; 661pp; English.

Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R94346;
02-UUL-1996 (first entry)
Hepatitis GB virus (HGBV) clone GB contig A protein prod.
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig A;
tamarin; infected plasma; lambda phage; cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                   Simons JN;
WPI; 95-293123/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buijk SI, Dawson GJ, Desai SM, Erker JC, Leary TP;
Muerhoff AS, Mushahwar IK, Pilot-Matias TJ, Schlauder GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codons in T00129" W09521922-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R94346 standard; Protein; 3164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1995; US-344557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference 1..3164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis GB virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "others correspond to degenerate or STOP
10 REKGHRPSHSC 20
                                                                                                                                             3164 AA;
                                                               Conservative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                       Score 57; DB 16; Length 3164; Pred. No. 3.21e+01;
                                                                    2; Mismatches
                                                                   3; Indels 0;
                                                                   Gaps
                                                                    0
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Search completed: Mon Mar 24 11:17:44 1997 Job time : 11 secs.

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Mar 24 11:16

US-08-644-289-1.rsp

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 24 11:18:31 1997; MasPar time 1.95 Seconds 190.205 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-1

Description: (1-20) from US08644289.pep

Perfect Score: 151

Sequence: 1 SLRPFKALVREKGHRPSHSC 20

Scoring table: PAM 150 Gap 15

Searched: 52205 seqs, 18531385 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot33
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10

8:part8 9:part9 10:part10

Mean 28.995; Variance 36.679; scale 0.791

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 2 3 3 4 4 6 6 6 7 7 10 11 11 12	Result No.
55 55 56 56 56 56 56 56 56 56 56 56 56 5	Score
42.4 41.1 40.4 39.7 39.7 39.7 39.7 39.7 39.7 39.7 39.7	Query Match
1166 164 231 237 256 466 466 1852 1873 2171 299 392 392 531	Length DB
1 9 8 8 10 4 2 2 2 2 3 3	DB
ADDB BACSU X16 HUMAN RMO5 PROWI GRAB_MOUSE YRNA ECOLI HEMZ_ARATH CIC1 CYPCA CIC1 RABIT CICC_RABIT CICC_RABIT YBBE YEASTI NOLC_RHIFR GILA_ORYSA KPK7_ARATH	ID
ATP-DEPENDENT NUCLEAS PRE-MRNA SPLICING FAC MITOCHONDRIAL 605 RIB GRANZYME B (G, H) PRECU HYPOTHETICAL 28.4 KD FERROCHELATASE, CHLOR DIHYDROPRYRIDINE-SENS DIHYDROPRYRIDINE-SENS DIHYDROPRYRIDINE-SENS UTAKTUR MITOCHONDRIA NOLC PROTEIN KINASE GILA (PUTATIVE SERINE/THREO	Description
2.47e-01 6.13e-01 9.57e-01 1.49e+00 1.49e+00 1.49e+00 1.49e+00 1.49e+00 1.49e+00 2.30e+00 2.30e+00 2.30e+00 3.53e+00	Pred. No.

ATP-BINDING; DNA REPAIR.
NP\_BIND 1 22

ATP (POTENTIAL).

\$8 38.4 609 5 KPK1 PRAVU PROTEIN KINASE PVPK-1 3.53e+00 \$7 37.7 193 9 VIF SIVCZ VIRION INFECTIVITY R 5.39e+00 \$7 37.7 193 9 VIF SIVCZ VIRION INFECTIVITY R 5.39e+00 \$7 37.7 502 9 WASP HUMAN WISKOTT-ALDRICH SYNDR 5.39e+00 \$7 37.7 502 1 B3AT CHICK BAND 3 ANION TRANSPOR 5.39e+00 \$7 37.7 610 5 LIN9 CAREL LIN-9 PROTEIN 5.39e+00 \$7 37.7 122 1 B3AZ RABIT ANION EXCHANGE PROTEI 8.18e+00 \$7 37.1 1234 1 B3AZ RABIT ANION EXCHANGE PROTEI 8.18e+00 \$8 37.1 1237 1 B3AZ RABIT ANION EXCHANGE PROTEI 8.18e+00 \$8 37.1 1237 1 B3AZ RABIT ANION EXCHANGE PROTEI 8.18e+00 \$8 37.1 1237 1 B3AZ RABIT ANION EXCHANGE PROTEI 8.18e+00 \$8 37.1 1237 1 B3AZ RABIT HISTONE H3.  \$8 4 328 10 YIAO HAEIN HYDOTHETICAL PROTEIN 1.23e+01 \$8 5 36.4 328 10 YIAO HAEIN HYDOTHETICAL PROTEIN 1.23e+01 \$8 5 36.4 386 8 SENR RAT PROBABLE G PROTEIN -CO 1.23e+01 \$8 5 36.4 386 4 GPRE RAT PROBABLE G PROTEIN-CO 1.23e+01 \$8 5 36.4 386 4 GPRE RAT PROBABLE G PROTEIN-CO 1.23e+01 \$8 5 36.4 828 9 V2A_TAV ZA PROTEIN (PROBABLE 1.23e+01) \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36.4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36 4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36 4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 36 4 1238 1 BVGS BORBE VIRULENCE SENSOR PROT 1.23e+01 \$8 5 4 124 1 DHP HUMAN CACADITATE DEHYDROGEN 1.85e+01 \$8 5 9 VGLB HSV2S GLYCOPROTEIN (CORE 1.85e+01 \$8 5 9 VGLB HSV2S GLYCOPROTEIN (CORE 1.85e+01 \$8 5 9 VGLB HSV2S GLYCOPROTEIN (SORE 1.85e+01 \$8 5 9 VGLB HSV2S GLYCOPRO	45	44	43	42	41	40	3 <b>9</b>	38	37	36	35	<u>34</u>	႘	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
193 9 KPKI PHAVU PROTEIN KINASE PVPK-1 1957 7 POL STYJL 193 9 VIF SIVOZ 193 9 VIF SIVOZ 193 9 VIF SIVOZ 193 9 VIF SIVOZ 201 193 9 VIF SIVOZ 201 193 1 POL POLYPROTEIN (CONT 202 1 PART 203 2 RABIT 203 203	54	54	54	54	54	54	54	54	55	55	55	55	55	55	55	55	55	55	55	55	55	56	56	56	56	57	57	57	57	57	58	58
1157 7 POL_SFV3L 1157 1	35.8	ავ			35.8	35.8	35.8		36.4		36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	37.1	37.1	37.1	37.1	37.7	37.7	37.7	37.7	37.7	38.4	38.4
POL SPV3L POLYDROTEIN KINASE PVPK-1 POL SPV3L POLYPROTEIN (CONT VIF SIVCZ VIRION INFECTIVITY FA PYRD ECOLI LIN9-GAEL LIN9-PROTEIN BAA2 RAT ANION EXCHANGE PROTEI BAA2 RATI ANION EXCHANGE PROTEI BAA2 MOUSE ANION EXCHANGE PROTEI HISTONE H3. PROCTOSE-BISHOSPHAFE SENE RAT PROBABLE G PROTEIN-CO GPRE RAT PROBABLE G PROTEIN-CO GPRE RAT LOW-DENSITY LIPOPROTE TRA PSEAE LOW-DENSITY LIPOPROTE TRA PSEAE TRA PSEA	2813	2131	885	811	605	452	239	202	1238	1238	_		879	828	586	436	386	386	364	328	134	1237	1237	1234	451	922	610	502	336	193	1157	609
PROTEIN KINASE PUPK-1 POL POLYPROTEIN (CONT VIRION INEECTIVITY FA DIHYDROOROTATE DEHYDR MYSKOTT-ALDRICH SYNDR LIN-9 PROTEIN. BAND 3 ANION TRANSPOR VIRULENCE SENSOR PROTEI ANION EXCHANGE PROTEI ANION EXCHANGE PROTEI ANION EXCHANGE PROTEIN FRUCTOSE-BISPHOSPHATE PROBABLE G PROTEIN-CO ADENOSYLMETHIONINE-8- OVERCOMING LYSOGENIZA ZA PROTEIN (PROBABLE LOW-DENSITY LIPOPROTE TRANSPOSASE FOR TRANS SULFITE REDUCTASE (NA VIRULENCE SENSOR PROT VIRUL	9 1	N	9	ω	2	4	10	œ	ᆫ	-	δ	9	S	9	9	_	4	œ	<u>,_</u>	10	4	<u> </u>		<b>-</b>	7	<b>,</b>	5	9	7	9	7	5
	VWF HUMAN	CINA DROME	VGLB HSV2S	GAG FOAMV	CACP HUMAN	IDHP HUMAN	YGGH_ECOLI	RR4 EPIVI	BVGS BORBR	BVGS_BORPE	MT10 YEAST	TRA PSEAE	LDLR RAT	V2A TAV	VOLD BPP2	BIOA MYCLE	GPRE RAT	SENR RAT	ALFB CHICK	YIAO HAEIN	H3 ENTHI	B3A2 MOUSE	B3A2 RABIT	B3A2_RAT	PHOQ SALTY	B3AT CHICK	LIN9 CAEEL	WASP HUMAN	PYRD ECOLI	VIF SIVCZ	POL SFV3L	
3.53e+00 5.39e+00 5.39e+00 5.39e+00 8.18e+00 8.18e+00 8.18e+00 1.23e+01 1.2			GLYCOPROTEIN B PRECUR	GAG POLYPROTEIN (CORE	CARNITINE O-ACETYLTRA	ISOCITRATE DEHYDROGEN	HYPOTHETICAL 27.3 KD	CHLOROPLAST 30S RIBOS	VIRULENCE SENSOR PROT	SENSOR P	SULFITE REDUCTASE (NA	TRANSPOSASE FOR TRANS				ADENOSYLMETHIONINE-8-	G	PROBABLE G PROTEIN-CO	FRUCTOSE-BISPHOSPHATE	HYPOTHETICAL PROTEIN	HISTONE H3.	EXCHANGE	EXCHANGE	ANION EXCHANGE PROTEI	-		•	WISKOTT-ALDRICH SYNDR			(CONT	PROTEIN KINASE PVPK-1
	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1,23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	1.23e+01	8.18e+00	8.18e+00	8.18e+00	8.18e+00	5.39e+00	5.39e+00	5.39e+00	5.39e+00	5.39e+00	3.53e+00	3.53e+00

# ALI GNMENTS

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SEQUENCE

1166

AA,

134631

M.

91EEB84F CRC32;

Mar 24 11:16 US-08-644-289-Lrsp

P46749; 01-NOV-1995 01-NOV-1995 01-NOV-1995 RPL5. RM05 PROTOTHECA WICKERHAMII. MITOCHONDRIAL PROWI (REL. 32, CREATED)
(REL. 32, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE) S09 STANDARD; RIBOSOMAL PROTEIN L5. 231 B

MITOCHONDRION.

CHLOROPHYCEAE; CHLOROCOCCALES; EUKARYOTA; PLANTA; PHYCOPHYTA; OOCYSTACEAE. CHLOROPHYTA (GREEN ALGAE);

STRAIN=263-11; SEQUENCE FROM N.A.

LANG B.F., KUECK U., BURGER G.;

MEDLINE; 94180393.
WOLFF G., PLANTE I., LANG B.F.
J. MOL. BIOL. 237:75-86(1994).

EMBL; U02970; G467861; -!- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.

RIBOSOMAL PROTEIN; MITOCHONDRION SEQUENCE 231 AA; 26584 MW; E827E483 CRC32;

PROSITE; PS00358; RIBOSOMAL\_L5

Query Match Best Local S Matches Similarity 7; Conservative 36.8%; 40.4%; Pred. Score 61; Mismatches No. 9.57e-01; DB 8; œ Length 231; Indels <u>.</u> Gaps

0

Ş В 88 lpaftalemitgqkpkytc 106 LRPFKALVREKGHRPSHSC 20

GRAB\_MOUSE P04187; STANDARD; 247 A

20-MAR-1987 (REL. 04, CREATED)
20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

GRANZYME B(G, H) PRECURSOR (EC 3.4.21.79) (CYTOTOXIC CELL PROTEASE 1) (CCP1) (CTLA-1) (FRAGMENTIN 2).

EUKARYOTA; METAZOA; MUS MUSCULUS (MOUSE). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

EUTHERIA; RODENTIA.

SEQUENCE FROM N.A.
MEDLINE; 86208120.
LOBE C.G., FINLAY B.B., PAI
SCIENCE 232:858-861(1986).

PARANCHYCH W., PAETKAU V.H., BLEACKLEY R.C.;

SEQUENCE FROM N.A. MEDLINE; 89062424.

MCFADDEN G., BLEACKLEY R.C. DUGGAN B., EHRMAN N. LETELLIER **X** 

BELL

J.

BIOCHEMISTRY 27:6941-6946(1988).

SEQUENCE FROM N.A.
MEDLINE; 86284960.
BRUNET J.F., DOSSETO M., DENIZOT F.,
HAQQI T.M., FERRIER P., NABHOLZ M.,
LUCIANI M.F., GOLSTEIN P.; DENIZOT F., CLARK W.R.,

, MATTEI M.G., CLARK W. SCHMITT-VERHULST A.M.,

NATURE 322:268-271 (1986)

US-08-644-289-Lrsp

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RESULT
ID YI
AC P
DT 00
DT 0
DT 0
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CN YI
CN YI
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                                                                                                                                                문
                                                                                                                                                                                                              Matches
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-40.
MEDLINE; 87215932.
MASSON D., TSCHOPP J.;
CELL 49:679-685(1987).
                                        01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                       CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
                                                                        YRDA ECO
P45770;
                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X04072; G50587; -.
EMBL; M12302; G309154; -.
EMBL; M22526; G201027; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. STRONGEST TO OTHER GRANZYMES AND TO MAST CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    > MET-|-XAA, SER-|-XAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURPHY M.E.P., MOULT J., BLEACKLEY R.C., GERSHENFELD WEISSMAN I.L., JAMES M.N.G.; PROTEINS 4:190-204(1988).
          ESCHERICHIA COLI
                     YRDA.
                              HYPOTHETICAL
                                                             01-NOV-1995
                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                            APOPTOSIS;
                                                                                                                                                                                                                                                                                                                                                      HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                     PIR;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A00956; PRMSCL.
PIR; A28952; A28952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ASP-|-XAA >> ASN-|-XAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89184501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELLING.
PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00135; TRYPSIN_SER.
                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-
                                                                                                                                                                              y Match 39.7%;
Local Similarity 38.9%;
                                                                                                                                                32
                                                                                                                             ω
                                                                                  ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER ASP. MAY BE INVOLVED
                                                                                                                            RPFKALVREKGHRPSHSC 20
                                                                                                                                              rpymallsikdqqpeaic 49
                                                                                                                                                                                                                                                                                                                                                                                     2CP1; 15-0CT-94.
                                                                                                                                                                                                                                                                                                                                                                                               B26944; B26944.
                                                                                                                                                                                                                                                                                                                                                                          PS00134; TRYPSIN_HIS.
                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                     SERINE PROTEASE; ZYMOGEN; SIGNAL; T-CELL; CYTOLYSIS;
                                                                                                                                                                                                             247 AA;
GRACILICUTES;
                             (REL.
(REL.
(REL.
28.4
                                                                                                                                                                                                                                  19
21
64
108
108
203
203
142
173
                                                                                                                                                                     Conservative
                                                                                   STANDARD;
                              8,22,32
                                                                                                                                                                                                                       18
20
247
64
108
203
203
209
188
71
                                                                                                                                                                                                             27470
                              PROTEIN IN RRND-AROE INTERGENIC REGION (0256)
                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                             CREATED)
                                                                                                                                                                                                              E
SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS
                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                               Pred. No. 1.49e+00;
                                                                                                                                                                                        Score 60; DB 4; Length 247;
                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM
                                                                                                                                                                     <u>ن</u>
                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                            GRANZYME B.
                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE.
                                                                                   PRT;
                                                                                                                                                                                                             E05916CB CRC32;
                                                                                                                                                                     Mismatches
                                                                                   256 AA
                                                                                                                                                                     6.
                                                                                                                                                                                                                                                                          (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOLYTIC
                                                                                                                                                                     <u>.</u>
                                                                                                                                                                     Gaps
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fnpltkrkdhrfprsc |::|:|| | ||::|| FKALVREKGHRPSHSC

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              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 39.7%;
Best Local Similarity 42.9%;
 Matches
                                                                                                                                                                                                                                                                                                                                                                        HEMZ ARATH

P42043;
01-NOV-1995 (REL. 32, GREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                    SMITH A.G., SANTANA M.A., WALLACE-COOK A.D.M., KUYEK J.M.,
LABBE-BOIS R.;
J. BIOL. CHEM. 269:13405-13413(1994).

J. CATALYTIC ACTIVITY: PROTOPORPHYRIN + FE(2+) = PROTOHEME + 2 H(+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECOGENE; EG12838; YRDA.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TRANSMEM 13 33 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12 / MG1655;
PLUNKETT G. III;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO P.AERUGINOSA FERRIPYOCHELIN BINDING PROTEIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U18997; G606213; -.
                                                                     CHAIN
                                                                                                                                                                                                                                                                    STRAIN=CV. LANDSBE MEDLINE; 94230447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTEROBACTER I ACEAE.
                                                                                                                                          EMBL; X73417; G511081; -.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             CAPPARALES; CRUCIFERAE.
                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE;
                                                       SEQUENCE
                                                                                   TRANSIT
                                                                                               TRANSIT
                                                                                                             PORPHYRIN BIOSYNTHESIS; HEME BIOSYNTHESIS; LYASE; IRON; CHLOROPLAST;
                                                                                                                           PROSITE; PS00534; FERROCHELATASE.
                                                                                                                                                       -!- SIMILARITY: TO OTHER SPECIES FERROCHELATASE
                                                                                                                                                                                                -!- PATHWAY: LAST STEP IN PROTOHEME BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                           ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                      -!- TISSUE SPECIFICITY: PRESENT IN BOTH LEAVES AND ROOTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 lrpyrdlfpqigqr
                                                                                                                                                                                    !- SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LRPFKALVREKGHR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.COLI PROTEIN CAIE.
                                                                                               PEPTIDE.
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 AA;
                                                       466 AA;
                                                                                                                                                                                                                                                                                   LANDSBERG ERECTA; TISSUE=WHOLE SEEDLINGS;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                      466
52032
              39.7%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28375 MW;
                                                                                   ٠.
                                                       MW;
              Score 60; DB 4; I
Pred. No. 1.49e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 10;
Pred. No. 1.49e+00;
                                                      FERROCHELATASE.
; 2D3756C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                  CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               725231B1 CRC32;
 Mismatches
                          Length 466;
4;
                                                                                                                                                                                                                                                                                                                                             DICOTYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                    (PROTOHEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
<u>,</u>
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US-08-644-289-1.rsp

STANDARD;

PRT;

1852 AA.

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CIC1 CYPCA STANDARI
P22316;
01-AUG-1991 (REL. 19, 0
01-AUG-1991 (REL. 19, 1
01-OCT-1993 (REL. 27, 1
                                                              TRANSMEM
TRANSMEM
CARBOHYD
CARBOHYD
                                                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DIHYDROPRYRIDINE-SENSITIVE L-TYPE, SKELETAL M
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-!- PTM: MAY NOT BE PHOSPHORYLATED.
-!- TISSUE SPECIFICITY: SKELETAL MUSCLE.
-!- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIHYDROPYRIDINE (DHP), A CALCIUM CHANNEL BLOCKER.
-!- SUBUNIT: THIS L-TYPE CALCIUM CHANNEL IS COMPOSED OF TWO SUBUNITS:
ALPHA-1, AND ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=SKELETAL MUSCLE; MEDLINE; 91126068.
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EXCITATION-CONTRACTION COUPLING. THE ALPHA-1 SUBUNIT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
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US-08-644-289-1.rsp

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US-08-644-289-1 rsp

SEQUENCE FROM N.A.

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902 lrplrainrakglkhvvqc 920

2 LRPFKALVREKGHRPSHSC 20

Matches

80

Conservative

Query Match 39.7%; Best Local Similarity 42.1%;

Score 60; MW;

DB 2;

Length 1873;

Pred. No. 1.49e+00;

Mismatches

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                                            FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
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(REL. 32, LAST ANNOTATION UPDATE)
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Pred. No. 1.49e+00;
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MEDLINE; 94378722.
HOLMSTROEM K., BRANDT T.,
YEAST 10:S47-S62(1994). KALLESOE T.;

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (POTENTIAL)

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

EMBL; X76053; G429137; -. EMBL; Z36160; G536746; -.

PIR; S44554; S44554. PIR; S39148; S39148.

PROSITE; PS00215; MITOCH\_CARRIER.

HYPOTHETICAL PROTEIN; MITOCHONDRION; INNER MEMBRANE; REPEAT;

PRANSMEM TRANSMEMBRANE; TRANSPORT.

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Query Match SEQUENCE 299 AA; ₹ CRC32;

Best Matches Local 39.1%; Similarity 50.0%; <u>.</u>, Conservative Score 59; DB 10; Length 299; Pred. No. 2.30e+00; 4; Mismatches 2; Indels <u>,</u> Gaps

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NOLC\_RHIFR P26508; STANDARD; PRT; 392

AA

01-AUG-1992 01-AUG-1992 01-NOV-1995 (REL. (REL. 23, CREATED)23, LAST SEQUENCE UPDATE)32, LAST ANNOTATION UPDATE)

NOLC PROTEIN

RHIZOBIUM FREDII

PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;

RHIZOBIACEAE.

SEQUENCE FROM N.A.

STRAIN=USDA257; MEDLINE; 91260457.

KRISHNAN H.B., PUEPPKE S.G.;

MOL. MICROBIOL. 5:737-745(1991). -!- SIMILARITY: TO PROKARYOTIC DNAJ, AND TO EUKARYOTIC DNAJ-LIKE PROTEINS.

EMBL; L03521; G152354; -. PIR; S15295; S15295.

PROSITE; PS00636; DNAJ\_NTER.

SEQUENCE DOMAIN DOMAIN DNAJ-LIKE. GLY-RICH. ARG-RICH.

Query Match Best Local Similarity 392 AA; 39.1**%**; 53.3%; 43565 MW; Score 59; DB 6; L Pred. No. 2.30e+00; CCD3D880 CRC32; Length 392;

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N LRPFKALVREKGHRP 16

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Query Match Best Local S Matches BINDING ACT\_SITE DOMAIN NON\_TER SEQUENCE NON\_TER LAWTON M.A., YAMAMOTO R.T., HANKS S.K., LAMB C.J.;
PROC. NATL. ACAD. SCI. U.S.A. 86:3140-3144(1989).
-!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF METABOLISM AND 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROTEIN KINASE G11A (EC 2.7.1.-) (FRAGMENT). G11A OR' P47997; NP\_BIND -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS EMBL; J04556; G169788; -STRAIN=CV. EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; MONOCOTYLEDONEAE; ORYZA SATIVA (RICE). TRANSFERASE; CYPERALES; GRAMINEAE. MEDLINE; 89240692. SEQUENCE FROM N.A. 01-FEB-1996 PROTEIN KINASES. STRONG, TO P.VULGARIS PVPK-1. SIGNAL TRANSDUCTION PROCESSES ORYSA Similarity œ 531 AA; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING (REL. 33, Conservative STANDARD; TISSUE=LEAF; 38.4%; 480 156 171 267 339 58647 MW; CREATED) PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
CYS-RICH INSERT. Pred. Score 58; DB 3; 2; Mismatches FAF6904A CRC32; PRT; No. 3.53e+00; 531 Ä <u>ب</u> Length 531; Indels OF SER/THR-<u>.</u>

268 lkpenvlvredgh |:| : |||| || 2 LRPFKALVREKGH 14 280 Gaps

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KPK7\_ARATH 13 STANDARD;

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Q059<del>9</del>9; PRT;

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01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PUŢATIVE SERINE/THREONINE-PROTEIN KINASE PK7 (EC 2.7.1.-).

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSP ANGIOSPERMAE; DICOTYLEDONEAE;

CAPPARALES; CRUCIFERAE.

SEQUENCE FROM N.A.

RESULT IN THE PROPERTY OF THE MEDLINE; 93077048.

HAYASHIDA N., MIZOGUCHI T., YAMAGUCHI-SHINOZAKI K., SHINOZAKI K., GENE 121:325-330(1992).

-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN ROOT TISSUE
WITH LOWER LEVELS FOUND IN LEAF, STEM, SEED AND FLOWER.

-!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-

EMBL; S50281; -; NOT\_ANNOTATED\_CDS. PROTEIN KINASES.

PIR; JC1385; JC1385.

SQ FT TT KW DR DR

DOMAIN

516 196

PROSITE, PS00107; PROTEIN KINASE ATP.
PROSITE; PS00108; PROTEIN KINASE ST.
PROSITE; PS0011; PROTEIN KINASE DOM.
TRANSFERASE; SERINE/THEONINE-PROTEIN KINASE; ATP-BINDING.

NP\_BIND BINDING ACT\_SITE SEQUENCE

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

578 AA; 182 188 211 307

9DB8E278 CRC32;

Mar 24 11.16

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RESULT
ID PC
AC P2
DT 01
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                                                                                                           В
                                                                                                                                  Matches
                                                                                                                                             Query Match 38.4%;
Best Local Similarity 61.5%;
POL_SFV3L STANDARD;
P27401;
01-AUG-1992 (REL. 23, CREATED)
                                                                                                                                                                                    NP_BIND
BINDING
ACT_SITE
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPK1 PHAVU STANDARD; PRT; 609 AA. P15792; P15792; O1-APR-1990 (REL. 14, CREATED) O1-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) O1-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) PROTEIN KINASE PVPK-1 (EC. 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                  LAWTON M.A., YAMAMOTO R.T., HANKS S.K., LAMB C.J.,
PROC. NATL. ACAD. SCI. U.S.A. 86:3140-3144(1989).
-!- SIMLLARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES. STRONG, TO RICE GIIA.
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                        PROSITE; PS00108; PROTEIN_KINASE_ST. PROSITE; PS50011; PROTEIN_KINASE_DOM.
                                                                                                                                                                                                                                                                                                                             EMBL; J04555; G169361; -. PIR; A30311; A30311.
                                                                                                                                                                                                                                                              TRANSFERASE;
                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP.
                                                                                                                                                                                                                                                                                                                  HSSP; P05132; 1CTP.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 89240692.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                       355 lkpenvlvredgh 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FABACEAE.
                                                                               |:| : |||| ||
2 LRPFKALVREKGH 14
                                                                                                                                  œ.
                                                                                                                                                                                    609 AA;
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                                                                                                                                                                                                                                                          SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.
                                                                                                                                  Conservative
                                                                                                                                                                                                565
243
258
258
354
421
                                                                                                                                                                                     68101
                                                                                                                                                                                  MW;
                                                                                                                                            Score 58; DB 5; Length 609; Pred. No. 3.53e+00;
                                                                                                                                                                                                         ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                 2;
                                                                                                                                                                                                CYS-RICH INSERT.
                              PRT;
                                                                                                                                                                                                                                                  PROTEIN KINASE.
                                                                                                                                                                                  A7E5A35F CRC32;
                                                                                                                                 Mismatches
                              1157 AA.
                                                                                                                                Indels
                                                                                                                              ç
                                                                                                                              Gaps
                                                                                                                             0;
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Search completed: Mon Mar 24 11:18:42 1997 Job time: 11 secs.

Q Ъ Matches Query Match 38.4%; Best Local Similarity 44.4%; ACT\_SITE SEQUENCE MEDIINE; 92124734.

RENNE R., FRIEDL E., SCHWEIZER M., FLEPS U., TUREK R.,

NEUWANN-HAEFELIN D.;

VIROLOGY 186:597-608 (1992).

-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. EMBL; M74895; G334872; -. PIR; B40820; GNLJLK. 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
POL POLYPROTEIN (CONTAINS: PROTEASE (EC 3.4.23.-);
TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE). ENDONUCLEASE; POLYPROTEIN. HYDROLASE; ASPARTYL PROTEASE; RNA-DIRECTED DNA POLYMERASE; 726 lkpdiiiihekghqptas 743 -!- THIS POLYPROTEIN IS PROBABLY SYNTHESIZED AS A GAG-POL POLYPROTEIN SPUMAVIRINAE. VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE; SIMIAN FOAMY VIRUS (TYPE 3 / STRAIN LK3) (SFV-3). SEQUENCE FROM N.A. 2 LRPFKALVREKGHRPSHS 19 BY A +1 FRAMESHIFT. 8 1157 AA; Conservative 38 131225 MW; Score 58; DB 7; I Pred. No. 3.53e+00; 6; Mismatches BY SIMILARITY. US-08-644-289-1.rsp C1425458 CRC32; 4; Indels Length 1157; REVERSE 0; Gaps <u>.</u>

S В

2 LRPFKALVREKGH 14

14

Query Match Best Local Similarity

38.4%; 61.5%;

Pred.

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Mismatches No. 3.53e+00;

μ

Indels

0;

Gaps

0;

Score 58;

DB 5;

Length 578;

Matches

8

Conservative

308 lkpenvlvredgh 320

Mar 24 11:16

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US-08-644-289-1 rpr

Release 2.1D John F. Coilins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 24 11:18:02 1997; MasPar time 2.66 Seconds 193.564 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-644-289-1 (1-20) from US08644289.pep 151

Scoring table: PAM 150 Gap 15 Sequence:

1 SLRPFKALVREKGHRPSHSC 20

82182 seqs, 25727515 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc 14:unrev

Statistics: Mean 27.793; Variance 45.751; scale 0.607

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result

esult No.	Score	% Query Match	% Query Match Length DB	D8	ID	Description	Pred. No.
<b></b>	65	43.0		14	S54125	pVIII protein - Avia	1.44e+00
2	64	42.4	1166	œ		ATP-dependent exonuc	2.08e+00
ω	62	41.1		12		X16 protein - mouse	4.32e+00
.4	62	41.1		12	A55645	voltage-dependent ca	4.32e+00
5	60	39.7		G	•	T-cell receptor beta	8.83e+00
6	6	39.7		<u>-</u>		cytotoxic T-lymphocy	8.83e+00
7	60	39.7		12	S12955	calcium channel prot	8.83e+00
∞	60	39.7		٩		ferrochelatase (EC 4	8.83e+00
9	60	39.7	1331	12	S05011	calcium channel alph	8.83e+00
10	60	39.7	1610	12	A46227	voltage-dependent Ca	8.83e+00
11	60	39.7	1646	12	JH0422	voltage-dependent ca	8.83e+00
12	60	39.7	1687	14	S41742	calcium channel alph	8.83e+00

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
56	56	57	57	57	57	57	57	58	58	58	58	58	58	58	58	58	58	58	58	59	59	59	60	60	60	60	60	60	60	60	60	60
37.1	37.1	37.7	37.7	37.7	37.7	37.7	37.7	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	38.4	39.1	39.1	39,1	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7
624 12	487 3	922 6	604 10		410 11	336 1		1157 3	. 609 9	586 9	578 9	531 9	480 8	444 11		131 5		115 5			299 9	299 10		2208 11		2171 12		2161 11	2143 12	2140 12		1873 12
S41688	VZEBPT	A30816	S15794	A55197	A44391	DEECDO	ASLJSI	GNLJLK	A30311	JN0505	JC1385	B30311	B61213	C55886	A45510	A27022	A41139	A36296	A30519	S15295	A55890	S44554	A45290	A37860	A38198	S05054	S11339	JH0564	JH0427	JH0426	A44467	A30063
DNA-binding protein	ler	3 anion tra	lin-9 protein - Caen			dihydroorotate oxida	protein - simi	/protein -	kinase	kinase	e e	protein kinase C (EC	ical prote	dopamine receptor D1		ם	n kinase 1	lreceptor	<pre>T-cell receptor beta</pre>	otein - Rhi	citrate transport pr		channel	channel	channel	channel	channel				voltage-dependent ca	dihydropyridine rece
	:-	2.51e+01		•	•		2.51e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.26e+01	1.26e+01	1.26e+01					8.83e+00		•			8.83e+00

# ALI GNMENTS

143 rpivrgrerrpprwc 159 ::    :::  ::  6 KALVREKGHRPSHSC 20	Qy 6 KALVRE
Query Match 43.0%; Score 65; DB 14; Length 245; Best Local Similarity 40.0%; Pred. No. 1.44e+00; Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;	Query Match Best Local Sim Matches 6;
##cross-references EMBL:X84724 Y #length 245	##cross-re SUMMARY
preliminary 1-245 ##label HES	##status
and organisation of the genome. \$54125	#accession
submitted to the EMBL Data Library, February 1995 The sequence of the two fibers of an avian adenovirus (CELO)	#submission #description
Hess, M.; Cuzange, A.; Chroboczeck, J.; Ruigrok, R.; Jacrot, B.	#authors
\$54125 \$54125	REFERENCE
08-Jul-1995	DATE
*formal_name Avian adenovirus	ORGANISM
S54125	TITLE
	RESULT 1

US-08-644-289-1 ppr

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Best Local Similarity 50.0%;
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Best Local Similarity 69.2%;
Matches 9; Conservative
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genes involved in ATP-dependent nuclease synthesis.
$cross-references_MJID:91267926
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                                                                                                       137 rslsrernhkpsrs 150
                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
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                                                                  6 KALVREKGHRPSHS
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                                                                                                                                                                                                                                                                 #superfamily ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                          A differentially expressed murine RNA encoding a protein with
                                                                                                                                                                                                                #length 164
                                                                                                                                                                                                                                                                                                                                               S14016
                                                                                                                                                                                                                                                                                                                                                                                                                Ayane, M.; Preuss, U.; Koehler, G.; Nielsen, Nucleic Acids Res. (1991) 19:1273-1278
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J. Bacteriol. (1991) 173:3644-3655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal name Bacillus subtilis
21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Mus musculus #common_name house mouse
18-Feb-1994_#sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #length 1166  #molecular-weight 134630  #checksum 5494
                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                           similarities to two types of nucleic acid binding motifs.
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                                                                                                                                                                                                                                                                                                          1-164 ##label AYA
                                                                                                                                                                                                             #domain ribonucleoprotein repeat homology #label
pth 164  #molecular-weight 19329  #checksum 8302
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                                                                                                                                                          Pred. No. 4.32e+00;
                                                                                                                                                                             Score 62; DB 12;
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    Mismatches

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A55645

#type complete

RESULT ENTRY

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#type complete

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                                                                                      Query Match 39.7%;
Best Local Similarity 53.8%;
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Best Local Similarity 42.1%;
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                                                                                                                                                                                                                                                                                                                                    #title
                                                                                                                                                                                                                                                                                                                                                                        #authors
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#map_position 1q31-q32
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                                                                                                                                                                                   ##note
                                                                                                                                                                                                      ##residues
                                                                                                                                                                                                               ##scatus preliminary; not compared with conceptual translation ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                902 lrplrainrakglkhvarc 920
                      12 likekgqrvnmsc 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LRPFKALVREKGHRPSHSC 20
LVREKGHRPSHSC 20
                                                                      7;
                                                                                                                                          the sequence was determined from the differentiated gene #superfamily immunoglobulin V region; immunoglobulin homology #length 116 #checksum 1551
                                                                                                                                                                                                                                                          E30563
                                                                                                                                                                                                                                                                                                          T cell receptor beta-chain genes in the rat. Availability and pattern of utilization of V gene segments differs from that
                                                                                                                                                                                                                                                                                                                                                                                                           E30563
                                                                                                                                                                                                                                                                                                                                                  Williams, C.B.; Gutman, G.A. J. Immunol. (1989) 142:1027-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                   #formal_name Rattus norvegicus #common_name Norway rat
03-Apr-1989 #text_change
                                                                      Conservative
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24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
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                                                                                      Score 60; DB 5; Length 116; Pred. No. 8.83e+00;
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GENETICS COMMENT

lymphocyte-specific serine proteases CCPI and CCPII. cross-references MUID:89062424 lymphocyte-specific genes. #cross-references MUID:86208120 cross-references MUID:86284960 ##cross-references EMBL:X04072 ##cross-references GB:M22526 ##molecule\_type\_DNA ##residues 1-247 ##label\_LO2 ##molecule\_type mRNA ##molecule\_type mRNA
#fresidues 1-247 ##label LOB ##cross-references GB:M12302 This enzyme is probably necessary for target cell lysis cell-mediated immune responses. Lobe, C.G.; Upton, C.; Duggan, B.; Ehrman, N.; Letellier, Bell, J.; McFadden, G.; Bleackley, R.C. Biochemistry (1988) 27:6941-6946
Organization of two genes encoding cytotoxic T chromosome mapping Brunet, J.F.; Dosseto, M.; Denizot, F.; Mattei, M.G.; Clark, Nature (1986) 322:268-271 Novel serine proteases encoded by two Science (1986) 232:858-861 CPPI; cytotoxic cell protease 1; cytotoxic T-cell-specific The inducible cytotoxic T~lymphocyte-associated gene Lobe, C.G.; Finlay, B.B.; Paranchych, W.; Paetkau, V.H.; A94288; A93382; A28952; A00956 #formal\_name Mus musculus #common\_name house mouse
04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change cytotoxic T-lymphocyte proteinase (EC 3.4.21.-) 1 precursor W.R.; Haqqi, T.M.; Ferrier, P.; Nabholz, M.; Schmitt-Verhulst, A.M.; Luciani, M.F.; Golstein, chromosome 14. transcript CTLA-1 sequence and gene localization to mouse Bleackley, R.C. 14-Jul-1994 1-247 ##label BRU #domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label APT\
#product cytotoxic T-lymphocyte proteinase 1 #status
predicted #label MPT\ cytotoxic T 'n ַ ACCESSIONS REFERENCE KEYWORDS DATE ENTRY TITLE Ş RESULT В ORGANISM DATE TITLE RESULT ENTRY SUMMARY Ş Ъ REFERENCE ACCESSIONS ORGANISM Matches Matches #accession #journal #authors #accession #title fauthors | journal ##status ##residues ##residues ##status 32 2 ω rpymallsikdqqpeaic 49 œ. 7;

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ORGANISM

ALTERNATE\_NAMES

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Mar 24 11:16 Conservative 5; US-08-644-289-1 rpr Mismatches 6 Indels 0; Gaps 0

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Query Match 39.7%; Best Local Similarity 42.1%; cross-references MUID: 91071434 ##eross-references EMBL:X58696
Y #length 347 #molecular-weight 40393 #checksum ##molecule\_type mRNA LRPFKALVREKGHRPSHSC 20 lrplrainrakglkhvvqc 25 RPFKALVREKGHRPSHSC 20 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change #formal\_name Arabidopsis thaliana #common\_name mouse-ear S12955 Smith, A.G.; Santana, M.A.; Wallace-Cook, A.D.M.; Roper, A54125 A54125 #type complete ferrochelatase (EC 4.99.1.1) precursor, chloroplast Polymerase chain reaction cloning of L-type calcium channel Huang, P.; Temizer, D.; Quertermous, T. FEBS Lett. (1990) 274:207-213 S12955 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change calcium channel protein type L - rabbit Conservative #formal J.M.; Labbe-Bois, R. 07-Jul-1995 Arabidopsis thaliana sequences from the heart and the brain. 10-Nov-1995 1-347 ##label HUA preliminary \_name Oryctolagus cuniculus #common\_name domestic #type complete Pred. No. 8.83e+00, Score 60; 4; Mismatches DB 12; Length 347; Indels <u>.</u> Gaps <u>,</u>

SUMMARY Query Match ##cross-references GB:X73417 ##molecule\_type mRNA chloroplast;
#length 466 A54125 J. Biol. Chem. Isolation of a cDNA encoding chloroplast ferrochelatase from Arabidopsis thaliana by functional complementation of a yeast mutant. 1-466 ##label SMI preliminary 39.7%; #molecular-weight 52032 #checksum (1994) 269:13405-13413 Score 60; DB 9; I Pred. No. 8.83e+00; DB 9; Length 466; 6060

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##experimental_source insulin-secreting cell line HIT-T15
##note sequence extracted from NCBI backbone
Y #length 1610 #molecular-weight 182326 #checksum 806
                                                               ##cross-references NCBIP:123692
                                                                                           ##residues
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##residues 1-1331 ##label SLI
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2 LRPFKALVREKGHRPSHSC 20
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                                                                                                                                                                                           Yaney, G.C.; Wheeler, M.B.; Wei, X.; Perez-Reyes, E.; Birnbaumer, L.; Boyd III, A.E.; Moss, L.G. Mol. Endocrinol. (1992) 6:2143-2152 Cloning of a novel alpha 1-subunit of the voltage-dependent calcium channel from the beta-cell.
                                                                                                                                                                                                                                                                                                             A46227
                                                                                                                                                                                                                                                                                                                                                                    #formal_name Mesocricetus auratus #common_name golden hamster
27-Oct-1993 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                   A46227 #type complete voltage-dependent Ca2+ channel alpha 1-subunit - golden
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Slish, D.F.; Engle, D.B.; Varadi, G.; Lotan, I.; Singer, D.; Dascal, N.; Schwartz, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S05011 #type fragment calcium channel alpha-1 chain, dihydropyridine sensitive, cardiac (clone HTDHP 2.0) - rabbit (fragment)
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    Mismatches

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RESULT

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RESULT Ş ORGANISM ₿ ACCESS IONS SUMMARY DATE ENTRY S ORGANISM В REFERENCE TITLE RESULT SUMMARY ACCESSIONS REFERENCE ACCESSIONS ORGANISM Matches Query Match 39.7%; Best Local Similarity 42.1%; Matches Query Match 39.7%; Best Local Similarity 42.1%; #title #authors #accession cross-references MUID:87258269 #accession #title # journal #authors 902 lrplrainrakglkhvvqc 920 ##residues ##molecule\_type mRNA 893 lrplrainrakglkhvvqc 911 ##residues ##status 2 LRPFKALVREKGHRPSHSC 20 2 14 13 LRPFKALVREKGHRPSHSC 20 = :: :: = :: **8**: œ #formal name Mus musculus #common name house mouse
31\_Dec-1993 #sequence\_revision 31\_Dec-1993 #text\_change #length 1873 #molecular-weight 212027 #checksum 5776 A44467 #type complete calcium channel complex alpha-1 chain mbC A30063 Nature (1987) 328:313-318
Primary structure of the receptor for calcium channel blockers from skeletal muscle. preliminary 1-1687 ##label GRA #length 1687 #molecular-weight 193873 #checksum Grabner, M.; Bachmann, A.; Rosenthal, F.; Striessnig, J.; Schulz, C.; Tautz, D.; Glossmann, H. FEBS Lett. (1994) 339:189-194 Tanabe, T.; Takeshima, H.; Mikami, A.; Flockerzi, 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change A30063 #formal 541742 Insect calcium channels. Molecular cloning of an alpha
(1)-subunit from housefly (Musca domestica) muscle. Conservative 541742 #formal\_name Musca domestica #common\_name house fly
25-Dec-1994 #sequence\_revision 25-Dec-1994 #text\_change calcium channel alpha-l-chain - House fly Conservative mouse 03-Mar-1995 T.; Numa, Takahashi, 18-Jun-1993 25-Dec-1994 1-1873 ##label TAN \_name Oryctolagus cuniculus #common\_name domestic #type complete H.; Kangawa, K.; Kojima, M.; Matsuo, Score 60; Pred. No. 8.83e+00; Pred. No. 8.83e+00, Score 60; 4; Mismatches Mismatches DB 12; DB 14; Length 1687; Length 1873; Indels 0; Indels0; V.; H.; Hirose, Gaps Gaps 0; 0

COMMENT DATE RESULT ENTRY REFERENCE REFERENCE ACCESSIONS TITLE Ş B ORGANISM SUMMARY KEYWORDS REFERENCE Matches Best Local Similarity 42.1%; Query Match #cross-references MUID:91299339
#accession JH0426 # journal #accession cross-references MUID: 90239020 #title #authors #title # journal **fauthors** #accession #title # journal cross-references MUID: 93054582 \*authors 1003 lrplrainrakglkhvvqc 1021 ##residues ##status ##molecule\_type mRNA ##experimental\_source brain ##molecule\_type mRNA ##note ##experimental\_source brain ##cross-references NCBIP:118042 ##molecule\_type mRNA ##residues 1-2139 ##label MA1 #cross-references GB:M57516 2 LRPFKALVREKGHRPSHSC 20 15 te the nucleotide sequence is not given Calcium channels are essential for many cellular functions, such as muscle contraction, propagation of action potentials, maintenance of electrical activity, and neurotransmitter regulation. 8 Davidson, N.

Proc. Natl. Acad. Sci. U.S.A. (1990) 87:3391-3395 Rat brain expresses a heterogeneous family of calcium C35901 Snutch, T.P.; Leonard, Distinct calcium channels are generated by alternative Ma, W.J.; Holz, R.W.; Uhler, M.D.
J. Biol. Chem. (1992) 267:22728-22732
Expression of a cDNA for a neuronal calcium channel alpha 1 subunit enhances secretion from adrenal chromaffin cells. Snutch, T.P.; Tomlinson, W.J.; Leonard, J.P.; Gilbert, M.M. Neuron (1991) 7:45-57 JH0426 JH0426; C35901 #formal\_name Rattus norvegicus #common\_name Norway rat
31\_Mar\_1992 #sequence\_revision 31-Mar-1992 #text\_change JH0426 #type complete voltage-dependent calcium channel complex alpha-1 chain rbC-I glycoprotein
#length 2139 #molecular-weight 240136 #checksum 8452 A44467 A44467 Conservative channels splicing and are differentially expressed in the mammalian 08-Feb-1996 1139-1384 ##label SN2 1-2140 ##label SNU preliminary; not compared with conceptual translation the codon for 1758-Tyr is TAA; the authors claim that sequence extracted from NCBI backbone clone contains TAC at this position this is an artifact of the cDNA cloning. Another cDNA 39.7%; Score 60; DB 12; Leng Pred. No. 8.83e+00; Wiematches 7; J.P.; Gilbert, M.M.; Lester, DB 12; Length 2139; 0; Gaps H.A.; <u>,</u>,

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SUMMARY 1818, 1898 #binding\_site phosphate (Ser) (covalent) #status
predicted
#length 2140 #molecular-weight 240188 #checksum 1204

Query Match 39.7%; Score 60; DB 12; Length 2140; Best Local Similarity 42.1%; Pred. No. 8.83e+00; Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps

0;

Db 1003 lrplrainrakglkhvvqc 1021 |||::|: | ||: | 0y 2 LRPFKALVREXGHRPSHSC 20

Search completed: Mon Mar 24 11:18:15 1997 Job time : 13 secs.

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SUMMARIES

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:41:07 1997; MasPar time 58.62 Seconds 533.919 Million cell updates/sec

Tabular output not generated.

Title: Perfect Score: Description: 38 (1-38) from US08644289.seq >US-08-644-289-2

N.A. Sequence: 1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38

Сотр: TCAGTCCGGAATCTCAATTTCCTACGGGTACGATGTCT

Scoring table: TABLE default Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Database:

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7 23:BCT8 24:BCT9 25:INVI 26:INV2 27:INV3 28:INV4 29:INV5 30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2 44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PRI1 51:PRI2 52:PRI3 53:PRI4 54:PRI5 55:PRI6 56:PRI7 57:PRI8 58:PRI9 59:PRI10 60:PRI11 61:PRI12 62:PRI13 63:ROD1 64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8 71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4 78:VRL5 79:VRL6 80:VRL7 81:VRL8 genbank 94 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PIN 9:PRI 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database: genbank-new5

82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL u-emb146\_94 96:part1

Database:

DEFINITION ACCESSION RESULT LOCUS

Murine gene for cellular tumour antigen p53 (exon 10).  $\chi_{0.0884}$ 

ALI GNMENTS

NID

g49989

SOURCE KEYWORDS ORGANISM

Mus musculus antigen.

house mouse.

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Statistics: Mean 7.583; Variance 2.828; scale 2.681

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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*: pnosphoreum JWA for Bacteriophage phi-X17 Bacteriophage phi-X17 Rat s-myc protein gen Mouse XRCC1 DNA repai	lymph node mRI sus monkey p53 an p53 gene fo -BR-E murine lam.	Human mRNA for mutate Human mRNA for mutate Human p53 cellular tu Human p53 cellular tu Human mRNA for p53 ce African Green Monkey Human mBNA fragment f Cat lymph node mRNA f Cat lymph node mRNA f	mRNA for mRNA for mRNA for mRNA for mRNA for mRNA for	Rattus norvegicus Wis Rattus norvegicus Wis Rat mRNA for nuclear Rattus norvegicus p53	0 1 →	
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KKSQHMTGVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306 (5943), 594-597 (1983)
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                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                         87064640
                                                                                                                                                                                                                                                                         Mol. Cell.
                                                                                                                                                                                                                                                                                          splicing
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                                                                                                                                                                                                                                                                                                         Immunologically distinct p53 molecules generated by alternative
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/usedin=X00876:P53_mRNA
1 25 c 35 g
              /db_xref="PID:g200201"
/translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL
LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG
                                                                                                                                  /sequenced_mol="cDNA to mRNA"
/tissue_lib="Meth A"
                                                                                                                                                                                      /strain="BALB/c"
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                                                                                                                                                                    /sub_species="domesticus"
                                                                                                                                                                                                      /organism="Mus musculus"
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nygfhlgflqsgtaksvmctyspplnklfcqlaktcpvqlwvsatppagsrvramaiy
                                                               /codon_start=1
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Pred. No. 4.28e-14;
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Best Local Similarity 100.0%;
Matches 34; Conservative
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Similarity 100.0%;
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                                                                                                                                                                                  FEMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD<sup>1</sup>
                                                                                                                                                                                                                                       KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
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                                                                                                                                                                                                                                                                                                                                                                                                    /sub_species="domesticus"
/cell_type="nontransformed helper T-cell"
                                                                                                                                                                                                                                                                           LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG
                                                                                                                                                                                                                                                                                              translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL/
                                                                                                                                                                                                                                                                                                             /product="p53 protein"
/db_xref="PID:g200199"
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Pred. No. 4.28e-14;
                                                                                          Score 34; DB 67;
Pred. No. 4.28e-14;
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Matches 34; Conservative
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Mol. Cell
                                                                           oncogene.
                                                                                                                                                         MMP53
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              Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
                                                                                               g53570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92253421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 20, 1979-1981 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arai, N., Nomura, D., Yokota, K., Wolf, D., Brill, E., Shohat, O. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                        Mus musculus
                                                        house mouse.
                                                                                                                     X00741
                                                                                                                                     Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 different tissue types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternatively apliced p53 rRNA in transformed and normal cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rotter, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Ab-MuLV transformed Meth A fibroblast and normal T-cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunologically distinct p53 molecules generated by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37064640
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                                                                                                                                     mRNA for transformation associated protein p53.
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Eumetazoa; Bilateria; Coelomata; Deuterostomia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEMFRELNEALELKDAHATEESGDSRAHSSLQPRAFQALIKEESPNC*
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="p53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="PID:g200203"
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Pred. No.
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 Chordata;
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LOCUS DEFINITION ij RESULT δ 밁 ORIGIN COMMENT REFERENCE ACCESSION FEATURES REFERENCE BASE COUNT REFERENCE SOURCE KEYWORDS AUTHORS TITLE TITLE AUTHORS TITLE MEDLINE ORGANISM Matches Query Match 89.5%; Best Local Similarity 100.0%; MEDLINE AUTHORS JOURNAL JOURNAL JOURNAL 1147 aggccttagagttaaaggatgcccatgctacaga 1180 CDS source 5 AGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 Mouse p53 cellular tumor antigen, mRNA. K01700 Jenkins, J.R., Rudge, K., Redmond, S. and Wade-Evans, J. Cloning and expression analysis of full length mousencoding the transformation associated protein p53 Nucleic Acids Res. 12 (14), 5609-5626 (1984) products and the adenovirus Ela proteins. All three of these proteins are rich in proline, contain proline runs or clusters, and are localized in the nucleus of transformed cells. The Ela proteins and p53 have been shown to have very short half-lives [2]. The Pennica, D., Goeddel, D.V., Hayflick, J.S., Reich, N.C., Anderson, C.W. and Levine, A.J. The amino acid sequence of murine p53 determined from a cDNA clone Virology 134, 477-482 (1984) A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983) Mus musculus DNA-binding protein; antigen; p53 gene; tumor antigen. Mouse embryo F9 carcinoma cells, cDNA to mRNA, clones p422, p208 [1], and clone pp53-1 [2]. sequence of cDNA in [1] The murine p53 protein is similar to the avian and human myc gene 86072076 84068204 Zakut-Houri, R., Oren, M., Bienz, B., Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; g200204 Data kindly reviewed (19-FEB-1986) by A. Wade-Evans. 84272240 Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 1377) Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Sutheria; (bases 105 to 1772) (bases 1 to 1716) 316 306, Conservative ø /codon\_start=1
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/translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL/translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDLLLPRDVEEFFEGPSEALRVSGAPAAQDDVTETPGQWPAPATPWPLSSFVPSGKTYQGN EMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD\* DRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKRF PEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGR KSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEP YGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYK /note="p53" Rodentia; Myomorpha; Muridae; Murinae. 23..1292 organism="Mus musculus" ...1377 ocation/Qualifiers 422 c 1772 bp Score 34; DB 64; Pred. No. 4.28e-14; 348 g 0; Mismatches was established by 291 t full length mouse and Wade-Evans, A. Lavie, V., Hazum, S. and Givol, D. **,**; Length 1377; ROD analysing Indels Glires; Rodentia; 03-MAY-1985 <u>,</u> cDNA sequences p176, Gaps Choanata; separate p271, <u>,</u> and

cDNA clones; p176 (bp 1-1247), p271 (bp 69-638), p422 (bp 1288-1719), and p208 (bp 1432-1719) [1]. There is only one functional p53 gene in the mouse genome.

p422

existing different forms of murine p53 must be products of the same

gene, mostly due to post-translational modifications [1]. The

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Best Local Similarity 100.0%;
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                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                         Mouse mRNA for cellular tumour antigen p53. X01237 K01700
Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306 (5943), 594-597 (1983)
                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                    Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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                                                                                                  Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                 antigen; tumor antigen.
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                                                                                                                            Tetrapoda; Amniota; Mammalia; Theria;
                                                                        (bases 1 to 1716)
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bp upstream of NcoI site.
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158..1330
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NYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIY
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/product="cellular tumor antigen"
/db_xref="PID:g200205"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 67;
Pred. No. 4.28e-14;
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                                                                                                       Murinae;
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Best Local Similarity 100.0%;
Matches 34; Conservative
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Analysis of the gene coding for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-NOV-1985) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ЕМВО J. 3 (9), 2179-2183 (1984)
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/citation=[1]
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Pred. No. 4.28e-14;
0; Mismatches 0;
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e murine cellular tumour antigen
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NID ACCESSION DEFINITION

g200206 K02110

Mouse p53 cellular tumour antigen psuedogene

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Best Local Similarity 100.0%;
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                                          Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                 g53574
                                                                                                                                                                                                      Mouse pseudoge
X01236 K02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              separate entry), and the psuedogene are almost identical from nucleotide 186 onward. Upstream of this position the two sequences deverge totally and no homology can be observed; downstream of here the two sequences differ by only 4%. The differences are due to substitutions and to some small deletions or additions in this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983)
                                                                                                                                                            antigen; pseudogene; tumor antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84068204
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Sciurognathi; Myomorpha; Muridae; Murinae; Mus
                                                                                                                  Mus musculus
                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                  MMP53P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relative to the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  introns, and is bounded by direct repeats (bp 169-181 and bp 1852-1864), suggesting that it is a processed gene which resulted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The DNA sequence of pCh53-11 contains a long poly-A tract, lacks
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                       Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
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Pred. No. 4.28e-14;
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Nature 306 (5943), 594-597 (1983)
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                                                                                                                                                                                                                                                        Structure of the rat p53 tumor suppressor gene Nucleic Acids Res. 21, 713-717 (1993)
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                                                                                                                                                                                                                                                                                                                    Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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1809..1814
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                                                                                                                                 /gene="p53"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (22-FEB-1994) Yue Lin, Department of Microbiology, National University of Singapore, Lower Kent Ridge Road, Singapore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 156 (2), 183-189 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin, Y. and Chan, S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                               National University of Singapore,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Rattus.
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                         /pseudo
540..640
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120..358
                                                                                                                                                        /gene="p53"
/note="corresponds
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                                                                                                                                                                                                                                                                                                                           /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                 /strain="Wistar"
/gene="p53"
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                                                                                                                  /gene="p53"
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                                                                                                                                                                                                                                                                                                                                         cell_type="hepatocyte"
                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
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                                                   note="corresponds
                                                             'gene="p53"
                                                                                                        note="corresponds"
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TITLE

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RESULT
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Matches 29; Conservativo
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                                                                                                                                                                                                                                                                                                                                                                                        X13058
                                                                                                                                                                   Submitted (26-SEP-1988) to the EMBL/GenBank/DDBJ databases. Soussi T., Universite Pierre et Marie Curie, Unite d'Oncologie Moleculaire, IRSC - CNRS, BP 08 94802 Villejuif, France
                                                                                                                                                                                                                                                                                                                                                                         g56828
                                                                                                                                                                                                                                                                                                                                                        oncoprotein p53.
                                                                                                                                                                                                                                                                                                                                                                                                                   RNP53
                                                                                                                            Nucleotide sequence of a cDNA encoding the rat p53 nuclear
                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                            Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                    Rat mRNA
                                                                       Data
                                                                                                   Nucleic Acids Res. 16 (23), 11384 (1988)
                                                                                                                  oncoprotein
                                                                                                                                           Soussi, T., Caron de Fromentel, C., Breugnot, C. and May, E.
                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                             Soussi,
                                                                                                                                                                                                                                                           Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                         Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                   Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
                                                                                      89083585
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                                                                       kindly reviewed (09-Feb-1989)
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/organism="Rattus norvegicus"
/cell_line="Py T21"
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Pred. No. 2.51e-05;
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RESULT ID NA ACC ID NA ACC
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Best Local Similarity
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16-MAR-1993 (Rel. 35, C
14-APR-1996 (Rel. 47, L
Rattus norvegicus p53 (
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                                                                                                                                                                                                                                                                                                                                                                                       misc_signal
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potential source of false 'mutations' in PCR fragments of tumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weghorst C.M., Buzard G.S., Calvert R.J., Hulla J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                       /note="this region of the pseudogene corresponds to exon of the rat p53 cDNA; putative" 2 \dots 4
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/codon_start=1
/db_xref="PID:956829"
/db_xref="PID:956829"
/translation="MEDSQSDMSIELPLSQETFSCLMKLLPPDDILPTTATGSPNSME
/trupquvaellegeeealqusapaaqeegteapavpaaarpmpisssypsgktyQ
GNYGFHLGFLQSGTAKSVMCTYSISLNKLFCQLAKTCPVQLMVTSTPPPGTRVRAMAI
                                                                                                                                                                                                         /note="this region of the pseudogene of the rat p53 cDNA; putative" 98..315
                                                                                                                                                 of the rat p53 cDNA; putative"
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  potential open reading
                                                                                    /gene="p53 PG-III"
                                                                                                                        <168..>542
                                                                                                                                                                                                                                                                                                                            /note="this site within the pseudogene
ATG translation start site of the rat p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="liver"
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                                                          /note=*tumor suppressor; this region of the pseudogene
                                                                                                                                                                                /note="this region of the pseudogene corresponds to exon 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Fischer 344"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
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85.3%;
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                                                                                                                                                                                                                                                                                                                               e corresponds to the p53 cDNA; putative"
NCBI gi: 206473"
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                                                                                                     Unpublished (1993)
                                                                                                                                                                                                                                                                   Rattus
                                                                                                                    the
                                                                                                                              Nucleotide sequence of a rat p53 pseudogene: a representative
                                                                                                                                           Weghorst, C.M., Buzard, G.S., Hulla, J.E., Calvert, R.J. and Rice, J.M.
                                                                                                                                                                                  Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                           tumor suppressor.
                                                                                                                                                                                                                                        g206472
                                                                                                                                                                                                                                                     L12046
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                                                                                                                                                                                                                                                                                                                                                                                                    52.6%;
Similarity 88.5%;
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                                                                                                                 family of p53 pseudogenes
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1107..1109
/note="this site within the pseudogene corresponds to translation stop site of the rat p53 cDNA; putative"
BP; 366 A; 388 C; 336 G; 357 T; 0 other;
                                                                                                                                                                                                                                                                 norvegicus
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       /tissue_type="liver"
                                    /sequenced_mol="DNA"
                                                /strain="Fisher 344"
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                        /sex="male"
                                                              organism="Rattus norvegicus"
                                                                            1..1447
                                                                                        Location/Qualifiers
                                                                                                                                                                     Rodentia; Myomorpha; Muridae;
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Pred. No. 3.66e-02;
                                                                                                                                                                                                                                                                 tumor suppressor pseudogene,
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RESULT 15  LOCUS RATPSEUDO 1447  DEFINITION Rattus norvegicus ACCESSION L12046  NID 9206472  KEYWORDS tumor suppressor. SOURCE Rattus norvegicus Eukaryotae; mitoc Vertebrata; Euthe Murinae; Rattus. REFERENCE 1 (bases 1 to 14	Db 976 gaattaaaggatg 	Query Match Best Local Similarity Matches 23; Conse	BASE COUNT 366 a	misc_signal	ехоп	exon	exon	exon	exon	exon			exon	exon	misc_signal
DDO 1447 bp DNA ROD 12-APR-1996 norvegicus p53 (PG-III) pseudogene, partial ORF.  puppressor. norvegicus (strain Fischer 344) DNA. norvegicus norvegicus tae; mitochondrial eukaryotes; Metazoa; Chordata; ata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; pres 1 to 1447)	gaattaaaggatgaccatgctgcaga 1001                            GAGTTAAAGGATGCCCATGCTACAGA 38	52.6%; Score 20; DB 69; Length 1447; arity 88.5%; Pred. No. 3.66e-02; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	PIOCESTAINS SITE WITHIN THE PSEUDOGENE COTRESPONDS TO THE translation stop site of the rat p53 cDNA; putative"  388 c 336 g 357 t	region of the pseudogene corresponds to exat p53 cDNA; putative"	region of the pseudogene corresponds 53 cDNA; putative"	region of the pseudogene corresponds to exon p53 cDNA; putative"	region of the pseudogene corresponds to exon p53 cDNA; putative*	his region of the pseudogene corresponds to exon at p53 cDNA; putative"	his region of at p53 cDNA;	 ID:g206473" n="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDN LAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHMTEVMRRCS PPPYPTPSILSG"	/note="this region of the pseudogene is a potential open reading frame; putative"	/note="this region of the pseudogene corresponds to exon 4 of the rat p53 cDNA; putative" <168>542	"this rat p	e="this site within th translation start site 97	region of the pseudogene corresponds to exp53 cDNA; putative*

Mar 25 02:40 US-08:644:289-2.rge

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BASE COUNT ORIGIN FEATURES COMMENT AUTHORS TITLE Query Match 52.6%; Best Local Similarity 88.5%; Matches 23; Conservative MEDLINE JOURNAL exon exon exon exon exon exon misc\_signal exon exon CDS exon misc\_signal source Weghorst, C.M., Buzard, G.S., Calvert, R.J., Hulla, J.E. and Rice, J.M. Cloning and sequence of a processed p53 pseudogene from rat: a potential source of false 'mutations' in PCR fragments of tumor DNA Gene 166 (2), 317-322 (1995) 96125211 366 อ 206472 /note="this site within the pseudogene corresponds to the translation stop site of the rat p53 cDNA; putative" a 388 c 336 g 357 t /note="this region of the pseudogene corresponds to exon of the rat p53 cDNA; putative" 1032..1447 /note="this region of the pseudogene corresponds to exon 10 of the rat p53 cDNA; putative" 1107..1109 /note="this region of the pseudogene corresponds to exon 6 of the rat p53 cDNA; putative" 747..882/gene="p53 PG-III" /note="this region of the pseudogene corresponds to exon of the rat p53 cDNA; putative" /gene="p53 PG-III"
/note="tumor suppressor; this region of the pseudogene is a potential open reading frame; putative; NCBI g1: 206473" /note="this region of the pseudogene corresponds to exon 8 of the rat p53 cDNA; putative" /translation="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDNQ VCYVHVLPSPKLAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHMTEVMRRCSH /note="this region of the pseudogene corresponds to exon
of the rat p53 cDNA; putative" /note="this region of the pseudogene corresponds to exon
of the rat p53 cDNA; putative" 938..1031 883..937 /note="this region of the pseudogene of the rat p53 cDNA; putative" 499..746 316..498 /note="this region of the pseudogene corresponds to exon 3
of the rat p53 cDNA; putative" /note="this site within the pseudogene corresponds to the ATG translation start site of the rat p53 cDNA; putative" HERCSDGDDQTPPPYPTPSILSG" /codon\_start=1 /db\_xref="PID:g206473" /tissue\_type="liver" /strain="Fischer 344" /sex="male" /organism="Rattus norvegicus" Location/Qualifiers Score 20; DB 91; L Pred. No. 3.66e-02; 0; Mismatches 3; Ų. Length 1447; Indels corresponds 0; Gaps ç exon 0;

Qy 13 GAGTTAAAGGATGCCCATGCTACAGA 38

Search completed: Tue Mar 25 02:42:11 1997 Job time : 64 secs.

Mar 25 02:42

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:43:09 1997; MasPar time 59.14 Seconds 283.363 Million cell updates/sec

Tabular output not generated.

Description: (1-38) from US08644289.seq 38 >US-08-644-289-2

N.A. Sequence: Perfect Score: 1 AGTCAGGCCTTAGAGTTAAAGGATGCCCATGCTACAGA 38 TCAGTCCGGAATCTCAATTTCCTACGGGTACGATGTCT

Scoring table: TABLE default

Gap

Nmatch STD: Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST17 28:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST33
23:EST33 34:EST34 35:EST25 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
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EST-STS-TWO 100:EST100 101:EST101 102:EST102 103:EST103 104:EST104 105:EST105 106:EST106 107:EST107 108:EST108 109:EST109 110:EST110 111:EST111 112:EST112 113:EST113 114:EST114 115:EST115 116:EST116 117:EST117 118:EST118 119:EST119 120:EST120 121:EST121 122:EST127 123:EST123 124:EST124 125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

Database:

141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST12 157:gnEST13 153:gnEST16 156:gnEST3 157:enEST3 158:enEST2 159:enEST3 159:enEST3 150:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8 165:enEST9 166:enEST10 167:enEST31 168:enEST112 173:enSTS1 174:enSTS2 169:enEST13 170:enEST14 171:enEST15 172:enEST16 130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7 136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1

Statistics: Mean 7.360; Variance 1.481; scale 4.970

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### o o KEYWORDS SOURCE ACCESSION DEFINITION 43 45 15 g1014189 H61357 yu41a06.r1 Homo sapiens cDNA clone 236338 5' similar to H61357 clone=236338 primer=M13RP1 library=Soares ovary tumor NbHOT 39.5 39.5 475 487 537 368 68 N71069 7 114 T46248 7 76 R15131 å ALIGNMENTS yf88c03.rl Homo sapie 5.03e-01 za86c10.s1 Homo sapie 9511 Arabidopsis thal 06-0CT-1995 5.03e-01 1 5.03e-01

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 368)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 284
Source: IMAGE Consortium, LLNL

BASE COUNT FEATURES source IMAGE 94 Consortium (info@image.llnl.gov) for further information. <1..>368 /organism="Homo sapiens" /clone="236338" Location/Qualifiers 99 с 109 g 61 , + S others

This clone is available royalty-free through LLNL ; contact the

Query Match 47.4%; Score 18; DB 25; Length 368; Best Local Similarity 79.3%; Pred. No. 9.68e-05; Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps

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RESULT LOCUS

HSC05H051

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EST

06-NOV-1994

ORIGIN

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mRNA BASE COUNT ç ORIGIN FEATURES COMMENT REFERENCE SOURCE KEYWORDS NID DEFINITION TOCUS. ACCESSION Best Matches Query Match AUTHORS ORGANISM source 292 tagaatgggcatcctttaa 310 34 Local TAGCATGGGCATCCTTTAA 16 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. repetitive element;. H97804 H97804 323 bp mRNA EST 12-DEC-1995 yw02f03.s1 Homo sapiens cDNA clone 251069 3' similar to contains High quality sequence stops: 240 Source: IMAGE Consortium, LLNL Unpublished (1995) Homo sapiens g1118689 Tel: 314 286 1800 Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Wilson, R. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Male. Email: est@watson.wustl.edu The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Albino. double-stranded cDNA was size selected, ligated to Eco RI adapters 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker human clone=251069 primer=m13 -40 forward library=Soares melanocyte 18; Similarity This clone is available royalty-free through LLNL; contact the (Pharmacia), digested with Not I and cloned into the Not I and Eco lst strand cDNA was primed with a Not I - oligo(dT) primer (bases 1 to 323) 139 Consortium (info@image.llnl.gov) for further information. Conservative മ <1..>323 a 66 c /note="human" /clone="251069" /organism="Homo sapiens" Location/Qualifiers 44.78; 94.78; 323 bp O Score 17; DB 36; Length 323; Pred. No. 1.89e-03; **.** 55 Mismatches g 61 4 1; Indels ~ others MO 63108 <u>,</u> Gaps <u>.</u> Ε

SOURCE NID

ORGANISM

REFERENCE

JOURNAL AUTHORS KEYWORDS

ACCESSION DEFINITION

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BASE COUNT ORIGIN

Query Match

Best Local

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Mar 25 02:42 US-08-644-289-2.rst

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DEFINITION ACCESSION REFERENCE ACCESSION BASE COUNT FEATURES KEYWORDS DEFINITION REFERENCE KEYWORDS Matches Query Match 42.1%; Best Local Similarity 73.5%; AUTHORS ORGANISM AUTHORS ORGANISM JOURNAL source 90 tagcaagtgcttcatttgactctacggttcgact 123 32 TAGCATGGGCATCCTTTAACTCTAAGGCCTGACT 1 Hillier,L., Clark,N., Dubuque,.., ---Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevask: human clone=117266 library=Stratagene lung (#937210)
vector=pBluescript SK- host=50LR cells (kanamycin resistant)
primer=-21m13 Rsitel=EccRI Rsite2=Xhol Normal lung tissue from a 7
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAC-3'; 3' adaptor sequence: Beier, D. and Brady, K. Unpublished (1995) R74999 Homo sapiens ye09902.s1 Homo sapiens cDNA clone 117266 3' similar to SP:PR22 YEAST P24384 PRE-MENA SPLICING FACTOR RNA HELICASE ;. Department of Pharmacology University of Colorado Health Sciences Center Mus musculus MDB0397R R74999 Eutheria; Primates; Catarrhini; Hominidae; g734809 T96185 T96185 Eutheria; Rodentia; Myomorpha; Muridae; Mus. 1 (bases 1 to 277) Eucaryotae; Metazoa; Chordata; using whole brain mRNA from a Balb C post natal 20 day. oligo-(dT) priming and directional cloning in Uni-ZAP XR The mouse brain library (Stratagene g849522 Eucaryotae; Metazoa; Chordata; 5'-CTCGAGTTTTTTTTTTTTTTTTT-3' Email: tjs@tally.hsc.colorado.edu. Tel: 3032708637 Box C236, Contact: Sikela JM host=E. coli XL1-Blue primer=M13 Reverse Rsite1=EcoR I Rsite2=Xho I house mouse library=Mouse brain, Stratagene vector=Lambda ZAP Fax: 3032707097 25; (bases 1 to 293) 71 a Conservative Mus musculus cDNA 5'end 1..277 /note="house mouse" Location/Qualifiers /organism="Mus musculus" 4200 E. 9th Ave, Denver CO 80262-0236 Clark, N., Dubuque, T., Elliston, K., Hawkins, M., 69 c 277 bp 293 bp Score 16; DB 93; Pred. No. 3.30e-02; 0 70 g mRNA Mismatches Vertebrata; Gnathostomata; Mammalia; Vertebrata; Gnathostomata; Mammalia; 66 t ) was constructed by 9 Length 277; EST 1 others Homo Indels 06-JUN-1995 Marra, M., 0; Gaps from a 72 <u>.</u>

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                      JOURNAL
                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yx31d08.s1 Homo sapiens cDNA clone 263343 3' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                          Hillier, L., Clark, N., Dubuque, T.,
                                                                                                                                                                                                                                    Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                      Unpublished (1995)
                                                                                                                Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human clone=263343 primer=m13 -40 forward library=Soares melanocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters
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                                            The WashU-Merck EST Project
                                                                                       Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                         foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P.
                                                                                                                                                                                                                                                                                                                                                                                                                              (Pharmacia), digested with Not I and cloned into the Not I and Eco
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/clone="117266"
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Pred. No. 3.30e-02;
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Best Local Similarity 76.7%;
Watches 23; Conservation
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L07332
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4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                Mus spretus-specific LINE-1 DNA probes applied to cloning of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus spretus (strain B6-spretus pe +Pin/pe +Pin) (library: EMBL3 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUSPROBEB
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                              Genomics 15,
                                                                                                                                                                                                                                                                                                                              murine pearl locus
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                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia; Myomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Animalia; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brad Rikke) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 325)
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a 61 c
             complement(304..325)
/note="PCR primer recommended to generate STS; putative"
a 69 c 54 g 107 t
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                                                                                                   order(1..21, complement(304..325))
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                                                                 /note="putative"
                                                                                                                     /note="PCR primer recommended to generate STS; putative"
                                                                                                                                                    tissue_lib="EMBL3 of Brad Rikke"
                                                                                                                                                                                                                          /strain="B6-spretus pe +Pin/pe +Pin"
                                                                                                                                                                                                                                          organism="Mus spretus"/
                                                                                 /map="chromosome 13"
                                                                                                                                                                     /sequenced_mol="DNA"
                                                                                                                                                                                                         /germline
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                    haplotype="pe +Pin"
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                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Mammalia; Theria;
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Query Match 42.1%; Best Local Similarity 83.3%; Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                            Genexpress_library_idt: C;
Genexpress_sequence_idt: y1c-3bh01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.P. 8, 94801 Villejuif Cedex France. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genexpress@genethon.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequence colinear to mRNA
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دو
                                                                                                                                                                                     Psychiatry Dept. Columbia University USA"
                                                                                                                                                                                                        /isolate="muscular atrophy patient"
/clone_lib="normalized infant brain cDNA from B.Soares,
                                                                                                     /dev_stage="3 months old"
45 c 62 g 119
                                                                                                                                             /tissue_type="total brain"
                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                 organism="Homo sapiens"
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                      Score 16; DB 44;
Pred. No. 3.30e-02;
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Location/Qualifiers
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 1 to 364)
Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C.,
                                                                                                                                                                                                                                                                           No significant homology found with :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5^{\prime} -> 3^{\prime} into the HindIII -> NotI sites of the lafmid BA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequence colinear to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing method: single read, full automatic;
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                   a
                                          /tissue type="total brain"
/clone lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                       /isolate="muscular atrophy patient"
                                                                                                                                                 /dev_stage="3 months old"
                                                                                                                                                                         /organism="Homo sapiens"
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195 tagaatgggtatccttgaactata 218

34 TAGCATGGGCATCCTTTAACTCTA 11

Matches

20;

Conservative

0;

Mismatches

Indels

<u>,</u>

Gaps

0

Pred. No. Score 16;

3.30e-02;

DB 40;

Length 364;

Query Match 42.1%; Best Local Similarity 83.3%;

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Best Local Similarity 83.3%;
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R57637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute, 100 College St., Toronto, Ontario, M5G1L5 Tel:
4169788758 Fax: 4169785650 Email: liewcc@utcc.utoronto.ca Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: GGTGGCGACGACTCCTGGAGCC. NCBI gi: 827695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Liew CC Molecular Cardiology University of Toronto Banting
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R57637
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F4425 Homo sapiens cDNA clone F4425 5'
                                      light chain.
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BP; 98 A; 75 C; 117 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Mar 25 02:42 US-08-644-289-2.rst

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REFERENCE AUTHORS Ş ORIGIN SOURCE rocns 맒 BASE COUNT COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION RESULT FEATURES SOURCE KEYWORDS TITLE TITLE ORGANISM Matches Query Match 42.1%; Best Local Similarity 83.3%; ORGANISM AUTHORS JOURNAL source 18 4 12 CAGGCCTTAGAGTTAAAGGATGCC 27 cagaccgtagagtttaaggaggcc 41 Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C. Analysis of expressed sequence tags from a fetal human heart cDNA g827695 EST. F4425 Hwang,D.M., Fung,Y.W., Wang,R.X., Laurenssen,C.M., Ng,S.H., Lam,W.Y., Tsui,K.W., Fung,K.P., Waye,M., Lee,C.Y. and Liew,C.C. Analysis of Expressed Sequence Tags (ESTs) from Fetal and Adult Heart cDNA Libraries Myosin alkali light chain. R57637 were ligated, followed by digestion with NotI, for direction cloning into predigested lambda gt22. Method is described in J. Mol. Cell. Cardiol. (1994) 26, 1329-1333). mRNA was purified from human fetal hearts (10-12 weeks). cDNA was constructed using a NotI-Oligo dT adaptor-primer. Sall adaptors Homo sapiens Banting Institute, 100 College St., Unpublished (1995) Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Homo sapiens human clone=F4425 library=Fetal heart vector=Lambda gt22 host=E. Molecular Cardiology Contact: Liew CC Genomics 30 (2), 293-298 Vertebrata; Eukaryotae; University of Toronto Molecular Cardiology Contact: Liew CC Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; coli Y1090 primer=GGTGGCGACGACTCCTGGAGCC Rsite1=NotI Rsite2=SalI library human. Fax: 4169785650 Tel: 4169788758 20; (bases 1 to 367) (bases 1 to 367) 86 Fetal heart Homo sapiens cDNA clone F4425 5' Conservative liewcc@utcc.utoronto.ca. ո /note="human" Location/Qualifiers /clone="F4425" /organism="Homo sapiens" mitochondrial eukaryotes; Metazoa; Chordata; Eutheria; Primates; Catarrhini; Hominidae; Homo 75 c 367 g Score 16; DB 88; Pred. No. 3.30e-02; 117 g 0; Mismatches mRNA 77 t Toronto, Ontario, M5G1L5 4; Length 367; Indels end similar to 02-MAY-1996 0; Gaps 0

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity 83.3%;
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                                                                                                                                                                                                                                                               Nishiguchi, S., Joh, T., Horie, K., Zou, Z., Yasunaga, T. and Shimada, K. A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells: characterization of low-abundance mRNAs
                                    Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g618877
EST(expressed sequence tag).
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Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758 .
                                                        3-1, Yamadaoka
Suita, Osaka, 565
                                                                                                                                       Division of Molecular Biomedicine
                                                                                                                                                                                    Kazunori Shimada
                                                                                                                                                                                                     Submitted (25-OCT-1993) to DDBJ by:
                                                                                                                                                                                                                                              J. Biochem. 116 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                 Phone: 06-879-8325
                                                                                              Osaka University
                                                                                                                      Research Institute for Microbial Diseases
                                                                                                                                                              Department of Medical Genetics
                                                                                                                                                                                                                            95096008
                                                                                                                                                                                                                                                                                                                                                                        Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
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Pred. No. 3.30e-02;
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ç 밁 Ş В RESULT ORIGIN BASE COUNT FEATURES Matches Matches Query Match 42.1%; Best Local Similarity 83.3%; Best Local Millasseau P., Marc S., Hazan J., Seboun E., Lathrop M.,
Gyapay G., Morissette J., Weissenbach J.;
"A comprehensive manetia ---Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: H.sapiens (D2S2334) DNA segment containing source Sequence 373 source Nature 380:152-154(1996). microsatellites" Jean.Weissenbach@genethon.fr Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases. Weissenbach J.; 1 - 373Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Homo sapiens (human) microsatellite marker; repeat polymorphism; STS. CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; AFM290zb5; single read. 22-MAR-1996 (Rel. 47, Z51281; HS290ZB5 full automatic; 18-MAR-1996 (Rel. 47, Created) A comprehensive genetic map of the human genome based on 5,264 80 catgggccacctttaaaattaaagcctg 107 31 5 00 CATGGGCATCCTTTAACTCTAAGGCCTG agaccttagagtacaaggctgccc 31 AGGCCTTAGAGTTAAAGGATGCCC 28 h 42.1%; Similarity 78.6%; 20; 22; standard; DNA; STS; 373 124 a /note="cloning vector is M13mp18"
BP; 132 A; 87 C; 53 G; 95 T; 6 other; Conservative Conservative /organism="Homo sapiens" /cell\_line="CEPH 134702" /clone\_lib="genomic DNA" 1..373 /chromosome="2" Location/Qualifiers Location/Qualifiers Last updated, Version 3) = Pred. No. 3.30e-02; Pred. No. 3.30e-02; Score 16; Score 16; 114 g **0**; 0; Mismatches Mismatches ВP DB 173; Length 373; DB 52; (CA) repeat; clone 4 6, Length 367 Indels Indels Mammalia; <u>,</u> 0 Gaps Gaps F9 0 <u>,</u>

JOURNAL COMMENT FEATURES REFERENCE AUTHORS REFERENCE AUTHORS TITLE RESULT LOCUS 유 SOURCE ACCESSION 문 BASE COUNT KEYWORDS DEFINITION Query Match 42.1%; Best Local Similarity 78.6%; Matches 22; Conservative TITLE ORGANISM JOURNAL 15 HSZY0ZB5 373 bp DNA STS 22-MAR-1996 H.sapiens (D2S2334) DNA segment containing (CA) repeat; clone AFM290zb5; single read. Nature 380, 152-154 (1996) Homo sapiens A comprehensive genetic map of the human genome based on 5,264 microsatellites Dib.C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A., Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyapay,G., Morissette,J. and Weissenbach,J. Direct Submission
Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
E-mail: Jean.Weissenbach@genethon.fr CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS. full automatic. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 373) g1232581 Weissenbach, J. human. (bases 1 to 373) 132 a /organism="Homo sapiens"
/note="cloning vector is M13mp18"
/cell\_line="CEPH 134702"
/clone\_lib="genomic DNA"
/chromosome="2"
2 a 87 c 53 g 95 t 6 c 1..373 Location/Qualifiers Score 16; DB 135; Length 373; Pred. No. 3.30e-02; 0; Mismatches 6; Indels 53 g 6 others Indels 0; Gaps **;** 

Search completed: Tue Mar 25 02:44:17 1997 Job time : 68 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:47:33 1997; MasPar time 8.73 Seconds 279.817 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-644-289-3 (1-28) from US08644289.seq 28

N.A. Sequence: 1 AGTCGAATTCATTGGGACCATCCTGGCT 28 TCAGCTTAAGTAACCCTGGTAGGACCGA

Comp:

Scoring table: TABLE default

Gap 10

Nmatch STD: Dbase 0; Query 0

113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

n-geneseq25
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.755; Variance 3.299; scale 1.744

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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16 16	16	16	16	20	23	28	Score
57.1 57.1	57.1	57.1	57.1	71.4	82.1	100.0	Query Match
303 303	280	184	184	91	91	28	% Query Match Length DB
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Q39930 Q59342	Q61255	Q59168	Q39756	Q51746	Q51746	T10487	ID
Expressed Sequence Ta Human brain Expressed	Human brain Expressed	Human brain Expressed	Expressed Sequence Ta	Oligonucleotide probe	Oligonucleotide probe	Human wild-type p53 g	Description
7.34e+00 7.34e+00	7.34e+00	7.34e+00	7.34e+00	4.74e-02	8.59e-04	7.90e-07	Pred. No.

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50.0			50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
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7 9 7 7					. 2											2 20		2 15			2					ω ω				9	2 8
Q75209 Q51024 Q44278	Q25591 T18877	Q71479 Q28568	Q14263	N71063	N70974	N92451	Q03369	Q11820	Q05617	Q59197	Q59313	N81164	Q36952	Q58708	T16883	T26961	T13451	Q92775	206900	N50531	N71120	N50521	Q55095	T11549	Q36395	N92579	Q31877	Q53209	Q59292	Q39880	Q61318
ALL-1 (acute lymphocy in Human FcERI beta chai in Serglycin - proteogly	Lipoxygenase structur Human TCL-1 gene.	Consensus sequence of Human thrombin recept		Genomic sequence enco	.,		Sequence encoding hum	ator	of porcine leu	ssed	Human brain Expressed	stituted E.co		coding se	ren			tin-ga	gene.		p.iq	q sal			nase g	•	n D3 pseudogene.	cyclin D3 pseud	in Express	Expressed Sequence Ta	Human brain Expressed 7
7.64e+01 7.64e+01 7.64e+01	7.64e+01 7.64e+01			7.64e+01		7.64e+01	7.64e+01	7.64e+01		7.64e+01	7.64e+01	7.64e+01	2.41e+01			2.41e+01	2.41e+01	2.41e+01		2.41e+01				7.34e+00	7.34e+00	7.34e+00	7.34e+00	7.34e+00	7.34e+00	7.34e+00	7.34e+00

## ALI GNMENTS

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gene. An epitope from intron 10 of the human p53 gene is used to	N-terminal (nucleotides -111 to 1090) portion of the wild-type p53	T10486-T10488 are primers used in a RT-PCR reaction to obtain an	Disclosure; Page 7; 40pp; English.	individual treatment regimes.	useful in diagnosis or prognosis of cancer, and for establishing	New antibodies specific for alternatively spliced mammalian p53 -	WPI; 96-140137/15.	Kulesz-Martin MF;	(HEAL-) HEALTH RES INC.	14-JUN-1994; US-259612.	05-JUN-1995; 150994.	15-DEC-1995.	CA2150994-A.	Homo sapiens.	reverse transcriptase polymerase chain reaction; ss.	proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle;	Tumour suppressor; p53; alternative splicing; antibody; cancer;	Human wild-type p53 gene N-terminal RT-PCR sense primer.	03-0CT-1996 (first entry)	T10487;	T10487 standard; DNA; 28 BP.	

US-08-644-289-3.rng

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US-08-644-289-3.mg

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RESULT
ID 05
AC 05
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Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.1%;
Best Local Similarity 0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ULT 2
Q51746 standard; cDNA; 91 BE
Q51746;
31-MAY-1994 (first entry)
Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                       88.
                                                                                                                                                                                                                                   LT 3
Q51746 standard; cDNA; 91
Q51746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shank DD, Spears WPI; 93-378844/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used in gene therapy of cancers and other proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of human cancer and in the study of p53 and alternatively spliced p53 (p53as) and their expression. When the antibodies are injected into cells they may cause cell cycle arrest. Vectors conty, p53as cDNA may
                                                                                                                                            Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                       Oligonucleotide probe MK14-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spliced p53. The antibodies are useful in the diagnosis and prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             create antibodies directed against this sequence in an alternatively
                                                                                                                                                                                                        31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection and amplification of Mycobacteria nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligo:nucleotide probes specific for Mycobacteria - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1993; 108325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BECT ) BECTON DICKINSON CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 9; Le
Pred. No. 8.59e-04;
25; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 21;
Pred. No. 7.90e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 91;
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AGCCAGGATGGTCCCAAT 11

unlike int directly int directly int directly int directly into the cost of th	for human genes actually transcribed in vivo. Unlike the random genomic DNA sequence tagged sites (STSs), ESTs point directly to expressed genes The use of ESTs could facilitate the tagging of most expressed human genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers Q39419-Q39580 (sequences designed from the ESTs) sublocalisation of an EST can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. This sequence represents EST0322.  Sequence 184 BP; 40 A; 52 C; 45 G; 47 T;  Sequence 184 BP; 51%; Score 16; DB 6; Length 184; tLocal Similarity 94.4%; Pred. No. 7.34e+00;
	Claim 3; Page 14; 23pp; English.  Claim 3; Page 14; 23pp; English.  Cliigonicleotide probe MK14-A consists of nucleotides 5-95 of MK14  (Q\$1735). It hybridized to all spp. of mycobacteria tested, but  cross reacted to a few non-mycobacterial spp. The probe may  be useful as an initial screen for mycobacterial infection.  See also Q\$135-5 and Q\$1747-59.  Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;  ry Match 71.4%; Score 20; DB 9; Length 91;  t Local Similarity 0.0%; Pred. No. 4.74e-02;  ches 0; Conservative 23; Mismatches 3; Indels 0; Gaps 0;  26 hswhhvyhhvysvyvyhhvyhby 51  :::::::::::::::::::::::::::::::::::

US-08-644-289-3 mg

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RESULT AC OFFICE OFFICE
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The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 6
Q61255 standard; DNA; 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on chromosomes, for individual or forensic identification, for mappi locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST00322 has a "poor" coding probability as evaluated using the
                                                                                                                                                                                                                             of most human genes
                                                                                                                                                                                                                                                                                                                                                                  Adams MD, Moreno RF, WPI; 93-272882/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09316178-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 132; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of most human genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      markers for human genes transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enriched oligonucleotides and corresp. sequences - used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams MD, Moreno RF, Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICE Adams MD, Moreno RF, Venter CJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9316178-A.
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                                                                                                                                                                                   Example 4; Page 462; 500pp; English.
                                                                                                                                                                                                                                                                           markers for human genes transcribed in-vivo, facilitate tagging
                                                                                                                                                                                                                                                                                                                Enriched oligonucleotides and corresp. sequences - used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1993; U01294.
12-FEB-1992; US-837195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain Expressed Sequence Tag EST01742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                061255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tagging of most human genes, for mapping locations of expressed genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1992; US-837195.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription; mapping; locations; chromosomes; chromosomal; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human brain Expressed Sequence Tag EST00322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-1993; U01294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 agccaggatggtctcaat 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCAGGATGGTCCCAAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93-272882/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 8; L
Pred. No. 7.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                <u>с</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in-vivo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 G;
        locations of expressed genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  facilitate tagging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ror mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                       Query Match 57.1%;
Best Local Similarity 94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.1%;
Best Local Similarity 94.4%;
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                          for human genes actually transcribed in vivo. Unlike the random genomic DNA sequence tagged sites (STSs), ESTs point directly to expressed genes. The use of ESTs could facilitate the tagging of most expressed human genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers 039419-039580 (sequences designed
            Human brain Expressed Sequence Tag EST00312.
Gene transcription product; genetic markers; tagging; in vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping chromosomes and tissue typing Claim 3; Page 189; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q39930 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coding-region prediction program CRM. Sequence 280 BP; 61 A; 62 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type, and for prepn. of antisense sequences, probes and constructs. EST01742 has a "poor" coding probability as evaluated using the
transcription; mapping; locations;
                                                                   Q59342;
                                                                                     Q59342 standard;
                                                                                                                                                                                                                                                                                          an analogous manner. This sequence represents EST00312. Sequence 303 BP; 102 A; 53 C; 67 G; 79 T;
                                                                                                                                                                                                                                                                                                                          from the ESTs) sublocalisation of an EST can be achieved with fragments from specific chromosomes or pools of large genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-1993.
19-JUN-1992; U05222.
20-JUN-1991; US-716831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed Sequence Tag human gene marker EST00312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on chromosomes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an EST (expressed sequence tag)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to transcription prods. of genes, useful for tagging genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Particular expressed sequence tags from human CDNA - corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 93-036325/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sublocalisation; gene tagging; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human gene sequencing; PCR mapping; somatic cell hybrids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; human genome project; chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           locations of disease-associated genes, for identification of tissue
                                                 l6-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹09300353-A.
                                                                                                                                                                       259 attgagaccatcctggct 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2-FEB-1992; US-837195
                                                                                                                                                      1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 agccaggatggtctcaat 61
                                                                                                                                                        ATTGGGACCATCCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCAGGATGGTCCCAAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC;
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for individual or forensic identification, for mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                   cDNA; 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7.34e+00;
                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16;
                                                                                                                                                                                                                                                        Score 16;
                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>.
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
chromosomes;
                                                                                                                                                                                                                                        7.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also Q59041-Q61440.
49 G; 107 T;
                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
                                                                                                                                                                                                                                                       Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 280;
                                                                                                                                                                                                                        l; Indels
                                                                                                                                                                                                                                                                                         79 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESTs are markers
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                             panels of
clones in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Homo sapiens. w09316178-A.

19-AUG-1993. 12-FEB-1993; U01294. 12-FEB-1992; US-837195.

Matches

17;

Conservative

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Mismatches 1;

Indels

<u>,</u>

Gaps

<u>.</u>.

Best Local Similarity 94.4%;

Pred. No. 7.34e+00;

US-08-644-289-3 mg

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RESULT OR ACTION OF THE STATE O S 맑 Query Match Matches type, and for prepn. of antisense sequences, probes and constructs. EST01770 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440. Sequence 342 BP; 60 A; 100 C; 88 G; 93 T; for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers  $\Gamma$ Example 4; Page 472; 500pp; English. Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss. Q61318; Q61318 standard; DNA; 342 BP type, and for prepn. of antisense sequences, probes and constructs. EST00312 has a "poor" coding probability as evaluated using the on chromosomes, for individual or forensic identification, for mapping for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes of most human genes WPI; 93-272882/34. Homo sapiens. WO9316178-A. Human brain Expressed Sequence Tag EST01770. See also Q59041-Q61440. coding-region prediction program CRM. The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers Example 1; Page 159; 500pp; English. of most human genes markers for human genes transcribed in-vivo, facilitate tagging Enriched oligonucleotides and corresp. sequences - used as WPI; 93-272882/34. Adams MD, Moreno RF, Venter CJ Adams MD, Moreno RF, Venter CJ. (USSH ) US DEPT HEALTH & HUMAN SERVICE 12-FEB-1993; U01770. 12-FEB-1992; US-837195. 16-MAR-1994 locations of disease-associated genes, for identification of tissue 9-AUG-1993. 259 attgagaccatcctggct 276 (USSH ) US DEPT HEALTH & HUMAN SERVICE. Watch 57.1%; Local Similarity 94.4%; H ATTGGGACCATCCTGGCT 28 17; 303 BP; (first entry) Conservative 102 A; Score 16; DB 8; L Pred. No. 7.34e+00; **°**; . 53 C; Mismatches 67 ç 1; Indels Length 303; 79 Τ; <u>.</u> for mapping Gaps 0;

Query Match

57.1%;

Score 16;

B

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Length 342;

Ş В ÷ Ъ Best Matches to transcription prods. of genes, useful for tagging genes, mapping chromosomes and tissue typing mapping chromosomes and tissue typing Claim 3; Page 171; 199p; English.
This sequence represents an EST (expressed sequence tag) ESTs are markers for human genes actually transcribed in vivo. Unlike the random genomic for human genes actually transcribed in vivo. from the ESTs) sublocalisation of an EST can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in an analogous manner. This sequence represents EST00337.

Sequence 406 BP; 103 A; 109 C; 114 G; 77 T; Q59292 standard; Q59292; DNA sequence tagged sites (STSs), ESTs point directly to expressed genes. The use of ESTs could facilitate the tagging of most expressed human genes within a few years at a fraction of the cost of complete genomic expressed sequence tag; human genome project; chromosome; Q39880 standard; DNA; 406 BP 12-FEB-1993; U01294. 12-FEB-1992; US-837195. (USSH ) US DEPT HEALTH & HUMAN SERVICE. Adams MD, Moreno RF, Venter CJ. WO9316178-A. Homo sapiens. transcription; mapping; locations; chromosomes; chromosomal; ss Gene transcription product; genetic markers; tagging; in vivo; Human brain Expressed Sequence Tag EST00337. sequencing. Using PCR primers Q39419-Q39580 (sequences designed Particular expressed sequence tags from human CDNA - corresponds WPI; 93-036325/04. 20-JUN-1991; US-716831. sublocalisation; gene tagging; tissue typing. human gene sequencing; PCR mapping; somatic cell hybrids; Expressed 20-MAY-1993 (first entry) 039880; Adams MD, (USSH ) US DEPT HEALTH & HUMAN SERVICE. 07-JAN-1993. VO9300353-A. 19-AUG-1993. 2-FEB-1992; 163 agccaggatggtctcaat 180 .6-MAR-1994 (first entry) 171 attgagaccatcctggct 188 9-JUN-1992; U05222 Local 11 ATTGGGACCATCCTGGCT 28 28 AGCCAGGATGGTCCCAAT 11 93-272882/34. h 57.1%; Similarity 94.4%; 17; Venter JC; Sequence Tag human gene marker EST00337. US-837195. Conservative cDNA; 406 Pred. No. 7 Score 16; 0 Mismatches DB 6; Length 406; .34e+00; 1; Indels 0 Gaps 0

US-08-644-289-3 mg

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RESULT
OF STATE OF ST RESULT 13 ID Q31877 standard; DNA; 2022 BP AC Q31877; Ş 밁 င္ပ 망 Query Match 57.1%; Best Local Similarity 94.4%; Query Match Matches Matches Query Match 57.1%; Best Local Similarity 94.4%; /\*tag= a W09324514-A. 09-DEC-1993. Q53209 standard; DNA; 2020 BP Disclosure; Fig 10; 108pp; English.
The sequence is that of a human cyclin D3 pseudogene.
Sequence 2020 BP; 553 A; 485 C; 463 G; 519 New D-type mammalian cyclin - replaces CIN-type protein needed for cell start in budding yeast and is detected by antibodies or D-type; mammalian; CLN protein; protein deficiency; cell cycle start; type, and for prepn. of antisense sequences, probes and constructs. EST00337 has a "poor" coding probability as evaluated using the on chromosomes, for individual or forensic identification, for mapping tagging of most human genes, for mapping locations of expressed genes The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate of most human genes Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging division hybridisation in biological samples to determine abnormal cell P-PSDB; R44806. WPI; 93-405720/50. Beach DH. 25-MAY-1993; U05000. 26-MAY-1992; US-888178. Homo sapiens. yeast; complement; ds. Human cyclin D3 pseudogene. 22-JUN-1994 Q53209 See also Q59041-Q61440. coding-region prediction program CRM. locations of disease-associated genes, for identification of tissue Example 1; Page 151; 500pp; English. (MITO-) MITOTIX. 171 attgagaccatcctggct 188 11 ATTGGGACCATCCTGGCT 28 17; 406 BP; Conservative (first entry) Conservative Location/Qualifiers 103 A; Score 16; DI Pred. No. 7. Pred. Pred. No. 7.34e+00, Score 16; <u>,,</u> 0; Mismatches 109 C; Mismatches DB 8; DB 9; ,34e+00; 114 G; 1; Indels Length 2020; Length 406; 1; Indels 77 T; 0 0 Gaps 0; 0;

밁 Query Match Best Local S Matches /\*tag= g /note= "A to ( W09220796-A. Recombinant mammalian D-type cyclin - replaces a CLN-type protein essential for cell start in budding yeast, its antibodies and probes being useful in detecting D-type cyclin in biological cycle or that they do not undergo destruction. The human cyclin D genes share very high similarity over their entire coding region: 60% Disclosure; Fig 10; 75pp; English.

The sequences given in Q31876-77 represents the cyclin D2 and D3 pseudogenes. These sequences were identified during the chromosomal localisation of the D2 and D3 genes. These genes were contained /\*tag= c /note= "Frameshift mutation" 1679 Sequence See also Q31873-75. but are less closely related than the cyclin A and cyclin E genes. The cyclin D genes are more closely related than the cyclin B genes between D1 and D2, different mechanism to govern their periodic degradation during cell and B-type cyclins which targets them for ubiquitin-dependant degradation. This suggests that the D-type cyclins have evolved a a similar small size protein ranging from 289-295 amino acids. novel D-type cyclins disclosed by this invention were shown to encode within clones lambdaD2-G1 and lambdaD3-G5 respectively. P-PSDB; R29314. WPI; 92-415774/50. Beach DH; /\*tag= /rpt\_type= Direct\_duplication
mutation 1182 /rpt\_type= Direct\_duplication
repeat\_unit 1379..1393 /\*tag= repeat\_unit /\*tag= d /note= "Frameshift mutation" /note= "Nonsense mutation" mutation 1210 mutation ubiquitin-dependant; degradation; similarity; D1; E; ss. Cyclin; D2; D3; Cyclin D3 pseudogene. 22-APR-1993 (COLD-) COLD 26-NOV-1992. repeat\_unit /\*tag= lack the "destruction box" identified in the N-terminus of both A-6-MAY-1991; 18-MAY-1992; U04146. ′\*tag= 827 agccaggatggtctcaat 844 Similarity 2022 BP; SPRING HARBOR LAB US-701514. (first entry) Conservative G mutation" 1361..1375 1134..1793 lambdaD2-G1; lambdaD3-G5; destruction box; A; 1265..1267 Location/Qualifiers 57.18; 94.48; 60% between D2 and D3 and 52% between D1 and D3. 554 A; Pred. No. 7.34e+00; 0; Mismatches 1 Score 16; 487 ς: DB 5; 463 G; Length 2022; The three 0; Gaps <u>.</u>

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28

AGCCAGGATGGTCCCAAT 11

T 14 N92579 standard; DNA; 3094 BP.

N92579;

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US-08-644-289-3 mg

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RESULT
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EP-34808 A.
06-DEC-1989.
02-UN-1989; 110056.
03-UUN-1988; US-202721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-1992 (first entry)
Sequence of the 1.7kb cDNA molecule encoding antibodies 7D1,7D4 and 20C6.
                             /note=
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                          T 15
036395 standard; DNA; 4721 BP.
036395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Fig 20A-D; 78pp; English.
The inventors claim a new protein which comprises one or more immunoreactive and/or antigenic determinants of an Eimeria surface antigen of mol. wt. 28,37,120 or more than 200 kD which specifically
                                                                                                                                   /note=
                                                                                                                                                            /*tag=
                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                          Benzene dioxygenase gene region.
Benzene; dioxygenase; cysbenzene glycol; transformation;
                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be enhanced by inserting additional genes into the carrier virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (see P93703-6). Also new are DNA encoding the protein (see N92576-9), and a vaccine comprising one or more proteins. Vaccine utility can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altenburger W, Binger MH, Chizzonite RA, Kramer RA, Lomedico PT, McAndrew SJ;
                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                         Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binds to one or more monoclonal antibody (MaB) from ATCC HB 9707-9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coccidiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pox:virus vectors as a vaccine to protect chicks against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences encoding Eimeria surface antigens - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; P93706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 89-358220/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eimeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; coccidiosis; poultry; bivalent vaccine; ss.
                                                                                                                                                                                                                   /note= "Benzene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN-LA ROCHE AG.
    *tag=
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                           "Benzene dioxygenase gene III"
3084..3413
                                                                                                                                   "Benzene
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ilarity 80.8%;
Conservative
                                                                                                        dioxygenase
2591..2998
                                                                                                                                                                                       dioxygenase gene 1912..2553
                                                                                                                                                                                                                                                                  Location/Qualifiers 499..1782
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Pred. No.
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                                                                                                                                   II,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 3; L
. 7.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              846 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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င့ DЬ Query Match 57.1%; Best Local Similarity 94.4%; Matches /note= "Benzene c -10\_signal / glycol dehydrogenase gene and catechol 2,3-oxygenase gene Claim 11; Page 12-18; 20pp; Japanese.
This sequence encodes five regions of a benzene dioxygenase (BDO) polypeptide. Cysbenzene gycol can be produced effectively from benzene using transformants prepared using this fragment.

Sequence 4721 BP; 917 A; 1382 C; 1494 G; 928 T; 1524 tggtcccaatgaaatcga 1541 WPI; 93-054795/07.
P-PSDB; R32085-89.
Microbe DNA - contg. benzene di:oxygenase gene, cis:benzene /\*tag= g J05003785-A. 30-ocT-1991; /\*tag= /note= [4-JAN-1993. SAOC ) MERCIAN CORP. 6-APR-1991; ·35\_signal 20 TGGTCCCAATGAATTCGA 3 "Benzene 284795. JP-084170. Conservative dioxygenase 479..484 dioxygenase 3410..4633 455..460 gene Score 16; DB 6; L Pred. No. 7.34e+00; gene IV" 0; Mismatches ۷, Length 4721; 1; Indels <u>,</u> Gaps 0

Job time : 15 secs Search completed: Tue Mar 25 02:47:48 1997

\* (MT

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:46:12 1997; MasPar time 54.01 Seconds 426.945 Million cell updates/sec

Tabular output not generated.

Title: Description: 28 >US-08-644-289-3 (1-28) from US08644289.seq

Perfect Score: N.A. Sequence: Comp: 1 AGTCGAATTCATTGGGACCATCCTGGCT 28 TCAGCTTAAGTAACCCTGGTAGGACCGA

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: Database: 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PIN 9:PRI 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7 23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:IVV4 29:INV5 30:INV6 31:INV7 32:MAN 35:MAN 35:MAN 35:VRT1 36:VRT2 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLN1 43:PLN2 44:PLN3 45:PLN4 46:PLN5 47:PLN6 48:PLN7 49:PLN8 50:PR11 51:PR12 52:PR13 53:PR14 54:PR15 55:PR16 56:PR17 57:PR18 58:PR15 59:PR110 60:PR111 61:PR112 62:PR113 63:RD11 64:RDD2 65:RDD3 66:RDD4 67:RDD5 68:RDD6 69:RD7 70:RD8 71:STR 72:SYN 73:UNA 74:VRL1 75:VRL2 76:VRL3 77:VRL4 genbank 94

Database: 78:VRL5 79:VRL6 80:VRL7 81:VRL8

genbank-new5
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG
89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL
u-embl46\_94

Database:

Statistics: Mean 7.337; Variance 2.794; scale 2.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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H. sapiens GbPD gene I Human DNA sequence fr Human DNA sequence fr Homo sapiens chromoso	sequence	Human DNA sequence fr	Human DNA sequence fr	Caenorhabditis elegan		cosmid N79E2.		rhabd	Human DNA from cosmid	DNA sequence	DNA sequence	gene for ATP	Human 4-hydroxyphenyl	K.oxytoca cym A, B, C, D	omonas sp. biph	Human DNA seguence fr	Down Syndrome	DNA sequence f	Down Syndrome	Na+, K+ A	Human thyroid peroxid	apiens (	-	,35	Homo sapiens (clones:		Brachydanio rerio (vh	R.americanum chioropi	Human DNA sequence fr		p53 celli		genomi	e qene fragment	Mouse tumor antigen p	Description	
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## ALIGNMENTS

ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	LOCUS	RESULT 1
Mus musculus Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;	Mouse DNA.	tumor antigen	g191973	M26862	Mouse tumor antigen p53 gene, 5' end.	MUSANTP53 536 bp DNA	
; Vertebrata;					5' end.	ROD	
Mammalia; Theria;						D 15-DEC-1989	

REFERENCE

AUTHORS TITLE

Bienz-Tadmor, B., Zakut-Houri, R., Libresco, S., Givol, D. and O: The 5' region of the p53 gene: Evolutionary conservation and evidence for a negative regulatory element

Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 536)

0 Gaps

0

JOURNAL MEDLINE REFERENCE

85027173

(bases 1 to 536)

EMBO J. 3 (9), 2179-2183 (1984)

TITLE

FEATURES

source

exon

MEDLINE JOURNAL AUTHORS REFERENCE AUTHORS

Bienz, B., Zakut-Houri, R., Givol, D. and Oren, M.

Muridae; Murinae; Mus.

(bases 1 to 536)

TITLE

LOCUS DEFINITION

MMANT01

536 ģ

DNA

NID

X00875 g49973

SOURCE **EYWORDS** ACCESSION

ORGANISM

Mus musculus

house mouse. antigen. Ş 뮹

426 ttcattgggaccatcctggct 446

8 TTCATTGGGACCATCCTGGCT 28

BASE COUNT ORIGIN

121

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156 c

120 g

139 t

/note="p53 mRNA" /organism="Mus musculus" 321..>536

mRNA

Query Match 75.0%; Best Local Similarity 100.0%; Matches 21; Conservative

Score 21; DB 65; Pred. No. 4.30e-03;

Length 536; Indels

Choanata;

<u>.</u>.

Mismatches

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0

FEATURES

source

MEDLINE

86135950 EMBO J.

4, 3209-3213 (1985)

Location/Qualifiers

JOURNAL

426 ttcattgggaccatcctggct 446

Query Match 75.0%; Best Local Similarity 100.0%; Matches 21; Conservative

Score 21; DB 63; I Pred. No. 4.30e-03; 0; Mismatches 0;

DB 63; Length 536; 0;

Indels

0;

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BASE COUNT

122

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155 c

120 g

139 €

/citation=[2] replace(288, "t")

conflict conflict

replace(157, "a") /citation=[2]

/usedin=X00876:P53\_mRNA

/label=exl

/organism="Mus musculus" Location/Qualifiers

Mar 25 02:45

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MEDLINE
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding protein; antigen; p53 gene; tumor antigen. Mouse embryo F9 carcinoma cells, cDNA to mRNA, clones p422, p208 [1], and clone pp53-1 [2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse p53 cellular tumor antigen, mRNA. K01700
                                                                                                                                                                                                                                                  sequence of cDNA in [1] was established by analysing four separate cDNA clones; p176 (bp 1-1247), p271 (bp 69-638), p422 (bp 1288-1719), and p208 (bp 1432-1719) [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                       separate entry), and the cDNA sequence are almost identical from nucleotide 186 onward. Upstream of this position the two sequences deverge totally and no homology can be observed; downstream of here the two sequences differ by only 4%. The differences are due to
                                                                                                                                                                                                                                                                                                                                      proteins are rich in proline, contain proline runs or clusters, and are localized in the nucleus of tranformed cells. The Ela proteins and p53 have been shown to have very short half-lives [2]. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennica, D., Goeddel, D.V., Hayflick, J.S., Reich, N.C., Anderson, C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g200204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSP53M
  substitutions and to some
                                                                                                                                      sequence of the murine p53 psuedogene, also reported by [1] (see
                                                                                                                                                                   gene, mostly due to post-translational modifications [1].
                                                                                                                                                                                                existing different forms of murine p53 must be products of the same
                                                                                                                                                                                                                             There is only one functional p53 gene in the mouse genome. All
                                                                                                                                                                                                                                                                                                                                                                                                                     products and the adenovirus Ela proteins. All three of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The murine p53 protein is similar to the avian and human myc gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86072076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 134, 477-482 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The amino acid sequence of murine p53 determined from a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Levine, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84068204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 105 to 1772)
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NYGFHLGF LQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIY
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/sequenced_mol="cDNA to mRNA"
113..1285
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/product="p53 protein"
/db_xref="PID:g200199"
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Pred.
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No. 4.30e-03;
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deletions or additions in this gene
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                                                                                                                                                                                      Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol A single gene and a pseudogene for the cellular tumour antigen Nature 306 (5943), 594-597 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse mRNA for cellular tumour antigen x01237 K01700
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                Givol, R.
                                                                                                                                   Bienz, B., Zakut-Houri, R., Givol, D. and Oren, M.
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Direct Submission
                                                      85027173
                                                                                                               Analysis of the gene coding for the murine cellular tumour antigen
                                                                                                                                                                           84068204
                                                                                                                                                                                                                                                                                                                             Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia;
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                                                                                                                                                                                                                                                                                                                                                                                                           antigen; tumor antigen.
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                                                                        ЕМВО J. 3 (9), 2179-2183 (1984)
                                                                                                                                                                                                                                                                      Sciurognathi; Myomorpha; Muridae;
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                                  (bases 1 to 1773)
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/map="11"
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<1..1668</pre>
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/product="cellular tumor antigen"
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Pred. No. 4.30e-03;
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Submitted (28-NOV-1985) to the EMBL/GenBank/DDBJ databases

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#### FEATURES COMMENT REFERENCE ORGANISM JOURNAL AUTHORS source repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region true left end of clone L185F6 is at 31621 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, constructed using flow-sorted human chromosome 4 from a Hamster-Human hybrid cell line ( $\tt UV20HL21-27$ ) containing human chromosomes 4, 8 and 21. L196E3 is contained in a clone contig spanning 2Mb which is described in Baxendale et al, Nature Cenetics 4 (1993) auspices of the U.S. Department of Energy. The library was such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the humpub@sanger.ac.uk Submitted (31-OCT-1995) Sanger Centre, Hinxton, Cambridgeshire, Direct Submission Williamson, H. Eukaryotae; VECTOR: sCos1 Genome Center, sequence is ambiguous, there is an annotation using the 'unsure' The true left end of clone L196E3 is at 1 in this sequence. submissions. shorter because we only sequence overlapping sections once, This sequence is not the entire insert of clone L196E3. IMPORTANT: CB10 1RQ, England. E-mail enquires regarding this sequence: Vertebrata; 6196E3 is from cosmid library LAO4NCO1 constructed at the Human eature key. longer because we arrange for a small overlap between neighbouring 218-230 181- 186. See also Myers et al, Cytogenet Cell Genet. 66 ( 1994 tebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 31720) /note="Alu 2575..4365 /note="MER42C element fragment" 4561..4854 /note="Alu repeat: matches 1..308 of consensus" 4252..4413 /note="Alu 1987..2278 /cell 1553..1846 958..1248 /clone\_lib="LA04NC01" 3462..3749 /note="MER42C element fragment" 3235..3459 3093..3146 /note="Alu 1262..1546 /note="Alu repeat: matches 1..308 of consensus" 323..612 229..319 /clone="L196E3" /map="4p16.3" /chromosome="4" /organism="Homo sapiens" Location/Qualifiers /note="MER42C element fragment" note="match: cDNA D25266" 'note="Alu repeat: matches 308..1 of consensus" /note="L1 element fragment" mitochondrial eukaryotes; Metazoa; Chordata; Los Alamos National Laboratory, NM 87545 under the line="UV20HL21-27" repeat: matches 308..1 of repeat: matches repeat: matches 1..308 of consensus 308..1 of consensus" consensus" It may be

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9498..9591
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8172..8342
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5744..5794
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23074..23108
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complement(14579..16027)
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6411..6582
/note="Alu repeat: matches 1..308 of consensus" 24223..24306
                                    /note="Alu repeat: matches 11..308 of
23768..24071
                                                                      /note="Alu repeat: matches 42..143 of 23258..23538
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14100..14303
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12416..12478
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10969..11257
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13742..13846
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                                                                                                                                                                                                                                                                                                                                                'note="MIR element fragment"
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/note="L1 element f
30243..30521
                                                                                                                                                                                                  /note="L1 element fragment"
30679..30805
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27610..27730
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27408..27523
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27248..27407
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25205..25361
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24590..24881
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24378..24527
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28142..28398
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28089..28134
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25853..26140
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24895..25202
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RESULT LOCUS

DEFINITION

CHRARBCL 914 bp DNA R.americanum chloroplast rbcL gene

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11-FEB-1994

ribulose-1,5-biphosphate-carboxylase and promoter region.

ACCESSION

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                                                                                                                                                                                                                                                          g496529
                                                                                                                                                                                                                                                                               X76109
                                                                                                                                                                                                                                                                                              A.anguilla mRNA for sodium/potassium ATPase, beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Savolainen, V.
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Cutler, C.P.
                                                      1 (bases 1 to 1147)
Cutler, C., Sanders, I.L. and Cramb, G.
                                                                                                                                    Vertebrata; Gnathostomata; Osteichthyes; Actinopterygii;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta
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                                   Unpublished
                                                                                                                                                       Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
                                                                                             Elopomorpha; Anguilliformes; Anguilloidei; Anguillidae; Anguilla.
                                                                                                                Actinopteri; Holostei; Halecostomi; Teleostei; Elopocephala;
                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
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/product="ribulose=1,5-bisphosphate-carboxylase"
/db_xref="PID:g12205"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chloroplast
/isolate="sample RA12"
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Ş Ъ FEATURES REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION **LOCUS** RESULT ORIGIN BASE COUNT FEATURES Query Match 60.7%; Best Local Similarity 90.5%; TITLE AUTHORS ORGANISM Matches TITLE MEDLINE JOURNAL JOURNAL CDS source source misc\_teature sig\_peptide 243 attcattggcaccatccaggc 263 7 ATTCATTGGGACCATCCTGGC 10 Brachydanio rerio (vhh-1) mRNA, complete cds. L27585 Brachydanio rerio Lane, Submitted (04-NOV-1993) to the EMBL/GenBank/DDBJ databases. C.P. Floor plate and motor neuron induction by vhh-1, a vertebrate Dodd, J Roelink, H., Augsburger, A., Heemskerk, J., Korzh, V., Norlin, S., Actinopterygii; Cypriniformes; 1 (bases 1 to 2600) Eukaryota; Animalia; Chordata; Vertebrata; Osteichthyes; zebrafish cDNA to mRNA. vertebrate hedgehog homologue; g452159 ZEFVHHIA Cutler, Direct Submission 94170375 homolog of hedgehog expressed by the notochord Cell 76 (4), 761-775 (1994) floor plate induction; motor neuron induction; 19; Altaba, A., Tanabe, Y., Placzek, M., Edlund, T., Jessell, T.T.M. 338 a yr, University of St. Andrews, St. Andrews, Fife, KY16, UK Conservative /tissue\_type="total embryo" /tissue\_lib="lambda ZAP-II" 320..388 /note="3' homologous region" a 277 c 261 g 271 t /translation="MPAATKDSDGGWKKFLWNSEKKEFLGRTGGSWAKILLFYVIFYG CLAGIFIGTIQALLLTINDFKPVYQDRVAPPGLSHTPRSEKSEMSFKVGDPSTYQKYV KAWHDFLQAYNDSKQENMMKYEDCGDTPKSYINRGELDNNQGIKKACIFRRSWLDKCS /tissue\_type="gill" 97..1008 1116..>1147 VYGQNIAYSDKDRYRGRFDVKFTINES" EEDAAKVREIKYYGIQEGFPLQYYPYYGKQLHPQYLQPLVAVHFTNLTMATELRIECR GLEDPTFGFSEGKPCLIVKLARIVNFRPRPPTSNDSIPEEAQSKVQPDVIPIYCTNKR /db\_xref="PID:g496530" subunit" /sequenced\_mol="cDNA to mRNA" 1..2600 /product="sodium /potassium-transporting ATPase, /EC\_number=\\_3.6.1.37\ /isolate="AnB1.1, Location/Qualifiers /gene="vhh-1" /dev\_stage="9-16 hours post fertilization" /organism="Brachydanio rerio" Location/Qualifiers /codon\_start=l 'gene="ATNB\_ANGAN" /organism="Anguilla anguilla" 2600 ģ Score 17; DB 35; Lenc Pred. No. 3.70e+00; "'omatches 2; 27 mRNA AnB2.13" Cyprinoidei; Cyprinidae. vhh-1 gene. Bute Medical Building, Westburn Length 1147; Indels 25-AUG-1994 <u>,</u> Gaps beta 0

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Best Local Similarity 87.0%;
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4p16.3.
Hamster-Human hybrid cell line ( \mbox{UV20HL}21\mbox{-}27 ) chromosomes 4, 8 and 21.
                                                    L30G1 is from cosmid library LA04NC01 constructed at the Human Genome Center, Los Alamos National Laboratory, NM 87545 under the auspices of the U.S. Department of Energy. The library was constructed using flow-sorted human chromosome 4 from a
                                                                                                                                                        The true left end of clone L30Gl is at 1 in this sequence. The true right end of clone L26El2 is at 21857.
The true right end of clone L30Gl is at 35473.
                                                                                                                                                                                                                                                                                             An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from cosmid L30G1, Huntington's Disease Region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-JAN-1996) Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
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                                                                                                                                                                                                                                                                  sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                        has been finished according to sequence map criteria as follows.
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone L30G1. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB10 1RQ, England. E-mail enquires: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heathcott,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ertebrata;
                                                                                                                                                                                                                                             eature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                  [MPORTANT:
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581 c 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPGDKVLAADSAGNLVFSDF IMFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSRLAVEAGFDWVYYESKAHIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDK LNS LA I SVMNHWPGVKLRVTEGWDEDGHHFEES LHYEGRAVD I TTSDRDKSKYGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MRLLTRVLLVSLLTLSLVVSGLACGPGRGYGRRRHPKKLTPLAY/
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Pred. No. 3.70e+00;
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                           containing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-1996
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FEATURES misc\_feature misc\_feature misc\_feature repeat\_region repeat\_region source repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region :epeat\_region L30C1 is contained in a clone contig spanning
2Mb which is described in Baxendale et al, Nature Genetics 4 ( 1993 181-186. /note="Alu repeat: matches 308..117 of consensus"
11991..12281 /note="Alu repeat: matches 1..112 of consensus"
11314..11483 /note="Alu repeat: matches
5638..6154 5393..5637 5085..5382 4618..4697 /note="Alu repeat: matches 308..1 of consensus"
4331..4708 2532..2824 /note="MLT2Al element fragment"
1779..2072 /cell /note="Alu repeat: 11793..11964 /note="Alu repeat: matches 11484..11775 11204..11314 385..629 /note="match: 5' 10115..10512 6661..6732 6533..6732 6361..6442 6265..6372 /note="L1 element fragment" 1172..1600 /31..1035 /note="match: 5' /clone lib="LA04NC01" /clone="L30G1" /map="4p16.3" /chromosome="4" /organism="Homo sapiens" /partial 'partial partial/ /note="match: multiple ESTs" /note="Alu repeat: matches 1..297 of consensus" 7325..7605 /note="MSTC element fragment" /note="MLT1A element fragment" /note="MSTC element fragment" /note="L1 element fragment" /partial /note="Alu /partial note="2 copies of 40 mer 95 % conserved" 'note="match: multiple ESTs" /partia /partia note="match: multiple ESTs" ocation/Qualifiers partial 'note="Alu See also Myers et al, Cytogenet Cell line="UV20HL21-27" repeat: matches repeat: matches 308..1 of consensus" EST R50568 clone 153110\* EST T68903 clone 82158\* matches 308..44 of consensus" 308..1 of consensus" 308..1 of consensus" 308..132 of consensus" Genet, 66 ( 1994

repeat_region repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region
198 1 Alu 213	/partial /note="Alu repeat: matches 3081 of consensus" 1940619697 /partial /note="Alu repeat: matches 3061 of consensus"		831 of consensus"	epeat: matches 1306 of co	2 mer 83 % cons	.17441 al "Alu repeat: matches 30888 of c	/note="Alu repeat: matches 1300 of consensus" 1679416975 /partial /note="Alu repeat: matches 123308 of consensus"	meat: matches 1155 of	/partial /note="Alu repeat: matches 3081 of consensus" 1635616494 /martial	<pre>/partial . /note="Alu repeat: matches 3081 of consensus" 1573316045</pre>	<pre>/partial /note="Alu repeat: matches 270308 of consensus" 1542815713</pre>	<pre>/partial /note="Alu repeat: matches 145185 of consensus" 1524915288</pre>	<pre>/note="Alu repeat: matches 1308 of consensus" 1476614802</pre>	<pre>/partial /note="Alu repeat: matches 81148 of consensus" 144814740</pre>	/partial /note="Alu repeat: matches 161 of consensus" 143814451	/partial /note="Alu repeat: matches 245308 of consensus" 1432314382	<pre>/partial /note="Alu repeat: matches 1246 of consensus" 1370813779</pre>	<pre>/note="Alu repeat: matches 1308 of consensus" 1277913009 /nartial</pre>	/note="Alu repeat: matches 3081 o 1248412776

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misc\_feature repeat\_region /note="Alu repeat: matches 1..308 of consensus"
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21654..21793 /note="Alu repeat: matches 17..308 of consensus"
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22026..22308 /note="Alu repeat: matches 308..135 of consensus"
21363..21653 /partial /partial /partial /partial /partial /partial /partia. partial matches 308..164 of consensus

Note: remainder of annotations omitted.

ငှ Db 32887 agcctggatggtcccaatg 32905 Query Match 60.7%; Best Local Similarity 94.7%; Matches 18; Conservative 28 AGCCAGGATGGTCCCAATG 10 Score 17; DB 54; Length 35473; Pred. No. 3.70e+00; 0; Mismatches 1; Indels 0 Indels 0; Gaps 0

LOCUS HUMTCRB 684973 bp DNA PRI 14-JAN-1995
DEFINITION Homo sapiens (clones: K41A, K35, K26, K56, X21B, G54, H137, H18, H18/G15gap, G15, X1A, A27, A212, A14, H7.1, H12.18, H130, A16, C215, G1, C68, C21, X11, X6A, C8G1, CBG1/C29gap, and C29) germline T-cell receptor beta chain, complete gene. KEYWORDS ACCESSION RESULT 12 C-beta gene segment; C-region; D-region; J-beta gene segment; J-segment; T cell receptor beta chain; TCR-beta gene; V-beta gene segment; V-segment; cell membrane protein; L36092 constant region; diversity region; germline; joining segment; trypsin; trypsinogen; variable segment. g540583

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REFERENCE AUTHORS REFERENCE SOURCE FEATURES AUTHORS TITLE TITLE ORGANISM MEDLINE JOURNAL JOURNAL source source repeat\_unit repeat\_unit repeat\_unit repeat\_unit repeat\_unit repeat\_unit repeat\_unit Homo sapiens (clone library: YAC D49H4) DNA; Homo sapiens (clone library: KAI Mang's) (tissue library: ATCC 1521) DNA; Homo sapiens (clone library: KAI Wang's) (tissue library: ATCC 1521) DNA; Homo sapiens (clone library: KAI Wang's) DNA; Homo sapiens (clone library: KAI Wang's) DNA; Homo sapiens (clone library: YAC 234 A6F6) DNA; Homo sapiens (clone library: YAC 234 A72B3) DNA; Homo sapiens (clone library: YAC 234 A72B3) DNA; Homo sapiens (clone library: YAC 234 A72B3) DNA; Homo sapiens (clone library: KAI Wang's) DNA; Homo sapiens Slightom, J.L., Siemieniak, D.R., Sieu, L.C., Koop, B.F. and Hood, L. Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor gene locus: direct primer-walking using cosmid template Homo sapiens Unpublished (1994) Sequence of the human T cell receptor beta locus Rowen, L., Koop, B.F. and Hood, L. 94292194 Genomics 20 (2), 149-168 (1994) Eutheria; Primates; Haplorhini; Catarrhini; Hominidae. Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; (bases 1 to 684973) (bases 368065 to 442094) /rpt\_family="Alu"
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/note="putative" /rpt\_family="Alu" 8317..8427 /rpt\_family="Alu" 2429..2988 complement (1..241)
/note="putative" /organism="Homo sapiens"
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repeat_unit	ource	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit	repeat_unit		source	repeat_unit	repeat_unit
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repeat\_unit

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'note="putative"

repeat\_unit

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Note: remainder of exon intron CDS exon exon ERNA repeat\_unit intron intron intron annotations omitted. /rpt\_family="Alu"
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Query Match 60.7%; Score 17; DB 61; Length 684973;

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REFERENCE AUTHORS TITLE SOURCE ORGANISM ₩ E P P R I B Ş Ş Db 523902 attgggaccatcctggc 523918 RESULT ORIGIN BASE COUNT FEATURES COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION Query Match 57.1%; Best Local Similarity 94.4%; Matches Matches JOURNAL TITLE AUTHORS Best Local X91841; 05-0CT-1995 (Rel. 45, Created) 22-APR-1996 (Rel. 47, Last updated, Version 5) H.sapiens DNA loop attachment sequence (clone LASO5) Alu sequence; loop attachment sequence. misc\_feature source repeat\_region HSLAS05SQ standard; DNA; PRI; 326 BP. 29 attgagaccatcctggct 46 11 ATTGGGACCATCCTGGC 27 11 ATTGGGACCATCCTGGCT 28 13 Jackson, D.A., Bartlett, J.M. and Cook, P.R. Sequence attaching loops of nuclear and mitochondrial DNA to underlying structures in human cells: the role of transcription Eukaryotae; | Vertebrata; H.sapiens DNA loop attachment sequence (clone LAS05).  $\times 10^{-10}$  X91841 Related sequence: Submitted (25-SEP-1995) P.R. Cook, Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, Direct Submission Cook, P.R. Homo sapiens NCBI gi: 1009421 J.Jurka, Proc.Natl.Acad.Sci.USA, 85, 4775-4778, 1988. Nucleic Acids Res. 24, 1212-1219 (1996) Alu sequence; loop attachment sequence g1009421 HSLAS05sQ human. Similarity 100.0%; 17; Conservative (bases 1 to 326) (bases 1 to 326) 118 a Conservative /note="DNA loop attachment sequences" 1 72 c 80 g 56 t /rpt\_family="Alu" <1..>326 /clone lib="DNA loop attachment sequences (LAS)"
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Homo sapiens (human) Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

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JOURNAL MEDLINE
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Best Local Similarity 94.4%; Pred. No. 1.76e+01;
Matches 17; Conservative 0; Mismatches 1
                                                                                                                         AUTHORS
                                                                                                                                                                                             ORGANISM
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Sequence 326 BP; 118 A; 72 C; 80 G; 56 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jackson D.A., Bartlett J.M., Cook P.R.;
"Sequence attaching loops of nuclear and mitochondrial DNA to underlying structures in human cells: the role of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-SEP-1995) to the EMBL/GenBank/DDBJ databases. P.R. Cook, Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OXI 3RE, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Related sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                11 ATTGGGACCATCCTGGCT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                29 attgagaccatcctggct 46
             Mutant U5A cells are complemented by an interferon-alpha beta receptor subunit generated by alternative processing of a new member of a cytokine receptor gene cluster EMBO J. 14 (20), 5100-5108 (1995)
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Homo sapiens (clone Q-20D3) interferon receptor (IFNAR2) gene, exon
                                                                                                                                                                                                                                                                                  g994719
                                                                                                   Lutfalla,G., Holland,S.J., Cinato,E., Monneron,D.,
Rogers,N.C., Smith,J.M., Stark,G.R., Gardiner,K., I
                                                                                                                                                         Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                               hematopoietin receptor family; interferon receptor.
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   96067138
                                                                                    Kerr, I.M. and Uze, G.
                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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                                                                                                   Mogensen, K.E.,
                                                                                                                         Reboul, J.,
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Mar 25 02:45 US-08-644-289-3.rge

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ORIGIN ç 밁 BASE COUNT FEATURES COMMENT Query Match 57.1%; Best Local Similarity 94.4%; Matches exon source exon intron 145 agccaggatggtctcaat 162 28 AGCCAGGATGGTCCCAAT 11 NCBI gi: 17; 237 a Conservative /number=5 582..754 /number=5 a 212 c /clone\_lib="LL2INCO2-Q" /map="21q22.1" order(L42239:1569..1661,1..581) 582..754 /gene="IFNAR2" /note="encodes SD100A s3-s7" /note="encodes SD100A s3-s7" /gene="IFNAR2" /number=4 /note="1.6 kB" /clone="Q-20D3" /macronuclear /organism="Homo sapiens" 'partial Location/Qualifiers Score 16; DB 90; I Pred. No. 1.76e+01; 200 g 0; Mismatches DB 90; Length 877; 228 t 1; Indels **,** 

Search completed: Tue Mar 25 02:47:15 1997 Job time : 63 secs.

Gaps

0;

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Mar 25 02:50

US-08-644-289-4 mg

W

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:52:36 1997; MasPar time 9.33 Seconds 280.530 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-08-644-289-4 (1-30) from US08644289.seq 30

N.A. Sequence: Сощр: 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30

TCAGCCTAGGACCTCACTCGGGACGACAGA

Scoring table: TABLE default Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: n-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22

Statistics: Mean 5.779; Variance 3.522; scale 1.641

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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17	17	17	17	19	20	21	24	No. Score
56.7	56.7	56.7	56.7	63.3	66.7	70.0	80.0	Query Match
1173	1062	984	471	34	91	1173	91	Query Match Length DB
5	11	11	11	21	9	12	9	DB
Q29632	Q62359	Q62361	Q62363	T10488	Q51746	Q67883	Q51746	ID
Hepatitis C virus HC-	Fragment coding for h	Fragment coding for h	Fragment coding for h	Human wild-type p53 g	Oligonucleotide probe	Murine p53 DNA.	Oligonucleotide probe	Description
3.91e+00	3.91e+00	3.91e+00	3.91e+00	3.63e-01	1.07e-01	3.08e-02	6.72e-04	Pred. No.

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		45	15	50.0	⊷ ( ⊷	076213	HSV L/ST

## ALI GNMENTS

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Sequence

See also Q51735-45 Sequence 91 BP;

and 5

9 Q51747-59. 5 A; 17 C

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15 DB 9;

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18 vvhvvshhhsvhhvvhhvhvsvvvvhhvvh 47 AGACAGCAGGGCTCACTCCAGGATCCGACT 1 

Matches Query Match

0:

Conservative

80.0%; 0.0%;

Score 24; Pred. No. 27; Misma

6.72e-04

Length

91;

Mismatches

Indels

<u>,,</u>

0

Best Local Similarity

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LT 2 Q67883

standard; DNA; 1173

ΒP

Q67883;

Murine p53 DNA.

23-MAR-1995 (first entry)

murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;

polymerase chain reaction; poxvirus; pSD542; immunological response; plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response; Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;

pathogen; human; interferon; IFN; ss.

21-JAN-1993; US-007115. 19-JAN-1994; US-184009.

21-JAN-1994; U00888. 04-AUG-1994. Synthetic

(VIRO-) VIROGENETICS CORP.

WPI; 94-263767/32

Cox WI,

Paoletti E, Tartaglia J;

Example 31; Fig 38; 232pp; English.

DNA encoding cytokine and/or tumour associated antigen Attenuated recombinant virus used for cancer therapy - comprises

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Mar 25 02:50

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30 AGACAGCAGGGCTCACTCCAG

10

US-08-644-289-4 mg

Ş В Matches Best Query Match Q51746 Q51746; create antibodies directed against this sequence in an alternatively spliced p53. The antibodies are useful in the diagnosis and prognosis of human cancer and in the study of p53 and alternatively spliced p53 Tumour suppressor; p53; alternative splicing; antibody; cancer; proliferative disorder; psoriasis; prognosis; diagnosis; cell cycle; Human wild-type p53 gene N-terminal antisense RT-PCR primer. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C 01-DEC-1993. 24-MAY-1993; 108325. 26-MAY-1992; US-889651. (BECT ) BECTON DICKINSON CO. Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; gene. An epitope from intron 10 of the human p53 gene is used to N-terminal (nucleotides -111 to 1090) portion of the wild-type p53 T10486-T10488 are primers used in a RT-PCR reaction to obtain an Disclosure; Page 7; 40pp; English. individual treatment regimes. useful in diagnosis or prognosis of cancer, New antibodies specific for alternatively spliced mammalian p53 WPI; 96-140137/15. Kulesz-Martin MF; 14-JUN-1994; US-259612. (HEAL-) HEALTH RES INC. 05-JUN-1995; CA2150994-A. Homo sapiens. reverse transcriptase polymerase chain reaction; ss. Tumour suppressor; p53; alternative splicing; 03-OCT-1996 (first entry) T10488; T10488 be useful as an initial screen for mycobacterial infection. cross reacted to a few non-mycobacterial spp. (Q51735). It hybridized to all spp. of mycobacteria tested, Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Claim 3; Page 14; 23pp; English. New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in WPI; 93-378844/48. Shank DD, EP-571911-A. Synthetic. Oligonucleotide probe MK14-A 31-MAY-1994 (first entry) samples .5-DEC-1995. Local 26 hsvhhvvhhvhvsvvvvhhvvhvvhhvhyh 55 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30 standard; standard; Similarity 0; Spears PA; Conservative DNA; cDNA; 91 66.7%; 34 ВP Score 20; DB 9; 1 Pred. No. 1.07e-01, 25; 17 C; Mismatches 15 G; and for establishing Length 5. 4 T; The probe may Indels 0; for Gaps 0;

US-08-644-289-4 mg

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RESULT
ID Q6
AC Q6
DT 18
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Best Local Similarity 100.0%;
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             Q62361;
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and here fragments.

and here fragments.
                                                                                                                                                                                                                                                                                                                          Non-radioactive detection of p53 specific antibodies - by capture on immobilised p53 or its fragments, then reaction with labelled second antibody, for diagnosis of tumours and suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 5
Q62363
Q62363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (p53as) and their expression. When the antibodies are injected into cells they may cause cell cycle arrest. Vectors contq. p53as cDNA may be used in gene therapy of cancers and other proliferative disorders
                         Q62361 standard;
                                                                                                                                                                                                                                                                                                                                                                                   Klein R, Schranz P, Tessmer C,
WPI; 94-135732/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragment coding for human p53 amino acids 237—393. Human nuclear phosphoprotein p53; tumour suppressor gene product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                         region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                   fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                                 Antibodies specific for p53 are detected by binding to immobilised
                                                                                                                                                                                                                                                                                               Claim 13; Page 25; 35pp; German.
                                                                                                                                                                                                                                                                                                              screening
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R51878.
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30-SEP-1992; DE-232823.
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/note= *partial CDS, therefore sequence does not
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/product= p53(237-393)
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18-NOV-1994
                                                                                               376 agcagggctcactccag 392
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                                                                                                                                         Conservative
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(first entry)
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                          cDNA; 984
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Pred. No. 3.91e+00;
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Ą. В Query Match Best Local S Matches each of these IIay... 984 BP; (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG. Klein R, Schranz P, Tessmer C, Volkmann M, WPI; 94-135732/16. Fragment coding for human p53 amino acids 40-393. Human nuclear phosphoprotein p53; tumour suppressor gene product; region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See Q62357-Q62366 for nucleic acid sequences coding for 30-SEP-1992; WO9408241-A. contain start or stop codons" /product= p53(40-393) /transl\_except= pos:700..702,aa:Arg /note= "partial CDS, therefore sequence Homo sapiens. anti-oncogene; cancer; tumour; antibody binding region; epitope; ds. Q62359 standard; Claim 13; Page 24; 35pp; German. second antibody, for diagnosis of tumours on immobilised p53 or its fragments, then Non-radioactive detection of p53 specific antibodies - by capture P-PSDB; R51876. Klein R, Schranz P, Tessmer C, Volkmann M, WPI; 94-135732/16. 30-SEP-1992; 30-SEP-1993; WO9408241-A. contain start or stop codons" /transl\_except= pos:622..624,aa:Arg
/note= "partial CDS, therefore sequence Homo sapiens. anti-oncogene; cancer; tumour; antibody binding region; epitope; ds. Human nuclear phosphoprotein p53; tumour suppressor gene product; Fragment coding for human p53 amino acids 66-393. 30-SEP-1993; fragments of the p53 gene product containing the antibody-binding Antibodies specific for p53 are detected by binding to immobilised (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG. 14-APR-1994. l8-NOV-1994 (first entry) 889 agcagggctcactccag 14-APR-1994. /product= p53(66-393) 26 AGCAGGGCTCACTCCAG Similarity 100.0%; 17; DE-232823. DE-232823. Conservative fragments. 1 BP; 224 A; Location/Qualifiers 1..1062 Location/Qualifiers cDNA; 1062 905 BP. Score 17; DB 11; Pred. No. 3.91e+00; ۰, 311 C; Mismatches does does not 259 G; and suitable reaction with 0: Length 984; Zentgraf Zentgraf H; 190 for Ε, labelled . . 0; Gaps 0

Claim 13; Page 22; 35pp; German.

screening

Non-radioactive detection of p53 specific antibodies — b on immobilised p53 or its fragments, then reaction with

by capture
 h labelled

second antibody, for diagnosis of tumours and suitable for

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Best Local Similarity 90.5%;
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Ubiquitin-conjugating enzyme; p53 protein; cell cycle; cell proliferation; cancer; psoriasis; fibrosia: da
                                                                                                                                                                                                                                                                                                                         oligo-nucleotide primers with nucleotide sequences corresp. to part. of the viral RNA Disclosure; Page 27; 54pp; English. This sequence represents the 3' region of hepatitis C virus RNA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1992.
23-APR-1992; 303625.
26-APR-1991; JP-191376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; primer; polymerase chain reaction; ss. Hepatitis C virus. EP-510952-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-1993 (first entry)
Hepatitis C virus HC-J1 3' region.
Non-A non-B hepatitis; NANBH; HCV; detection; diagnosis; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GT 8
Q29632 standard; DNA; 1173
Q29632;
                          Human p53 cDNA.
                                           06-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                was isolated from several samples and homology compared, and the respective sequence of about 1900-2500 nucleotides of the 5^{\prime}
                                                                                                                                                                                                                                                                                                             This sequence represents the 3' region of hepatitis C virus RN original sample was obtained from human and chimpanzee plasma.
                                                          Q97854;
                                                                         Q97854
                                                                                                                                                                                                                                                                                                                                                                                      Detection of non-A, non-B hepatitis virus - using new
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 92-359137/44.
                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura T, Okamoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               each of these fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368-386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies specific for p53 are detected by binding to immobilised fragments of the p53 gene product containing the antibody-binding
                                                                                                                                                                                                                                                                     terminus
                                                                                                                                                516 agacagcaaggcacactccag 536
                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMO ) IMMUNO JAPAN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           967 agcagggctcactccag
                                                                                                                                  မ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 AGCAGGGCTCACTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 56.7%;
Local Similarity 100.0%;
les 17; Conservative
                                                                                       9
                                                                                                                                  AGACAGCAGGGCTCACTCCAG
                                                                        standard;
                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                 and 1100 nucleotides of the 3' terminus determined.

1173 BP; 248 A; 348 C; 305 G; 272 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See Q62357-Q62366 for nucleic acid sequences coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1062 BP;
                                                                                                                                                                                           Conservative
                                                                        cDNA; 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 A;
                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뭐
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 11; Length 1062; Pred. No. 3.91e+00;
                                                                         ВP
                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                        Score 17;
                                                                                                                                                                                          <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 C;
                                                                                                                                                                                                          3.91e+00;
                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 G;
                                                                                                                                                                                                                       Length 1173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 T;
                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 agcagggctcactccag 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-1994;
27-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wild type p53 gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T29719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant p53 in Sf9 insect cells for use as a component of an in vitro ubiquitin conjugating system.

Sequence 1181 BP; 275 A; 366 C; 306 G; 234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating
P-PSDB; R91933.
Use of wild-type p53 gene - in a medicament for suppressing neoplastic phenotype of a cancer cell lacking wild-type p53 Claim 1; Page 5; 25pp; English.
                                                                                                                        Chen P, Lee W; WPI; 96-223439/23.
                                                                                                                                                                                                                  24-AUG-1990;
                                                                                                                                                                                                                                                                             08-MAY-1996.
                                                                                                                                                                                                                                                                                                       /transl_except=
EP-710722-A1.
                                                                                                                                                                                                                                                                                                                                                                                           /product= p53 protein.
misc_difference 19..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bladder cells; prostate carcinoma cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteosarcoma cells; lung carcinoma cells; lymphoma cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p53 gene; cancer; carcinoma; neoplastic; neoplasia; phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was subcloned into a baculovirus vector for expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human p53 cDNA (given in Q97854) was amplified from a HeLa cell cDNA library using the primers given in Q97852-53. The gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. cell proliferation
Disclosure; Page 105-106; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R79658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 95-255137/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cottarel G, Draetta G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09518974-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                              23-AUG-1991; 307791
                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia cells; soft tissue sarcoma cells; breast cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-1994; US-305520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AGCAGGGCTCACTCCAG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA; 1182 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-247904.
US-250795.
                                                                                                                                                                                                                  US-573405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                      CAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eckstein JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 15;
Pred. No. 3.91e+00;
                                                                                                                                                                                                                                                                                                                                   Aspartic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rolfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULTION OF COLUMN AND COLUMN AN
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မွ
                                                                       문
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Best Local Similarity 100.0%;
                                                                                                                                                                     Query Match 56.7%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                           Matches
                                                                                                                                                                                                                                                               mutant p53 gene was obtained from plasmid Cx22A and cloned into pMM110 to generate pMM143. Recombination between pMM143 and ALVAC rescuing virus produced recombinant virus vCP270, which contains the vaccinia H6 promoted mutated human p53 in the C5 locus. The resulting virus may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens.

Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T;
for suppressing the neoplastic phenotype of a cancer cell lacking endogenous wild type p53 protein. Cancer cells suppressed in such fashion include osteosarcoma cells, lung carcinoma cells, lymphoma cells, leukaemia cells, soft tissue sarcoma cells or breast, bladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The plasmid pMM110 (see also Q67864) contains the vaccinia H6 promoter and the wild type human p53 gane in the ALVAC C5 insertion site. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cox WI, Paoletti WPI; 94-263767/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1994; U00888.
21-JAN-1993; US-007115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    murine; interleukin-2; II-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
plasmid; vaccinia; H6 promoter; amplify; primer; antiqenic response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      position 524, changing an Arg residue at position 175 to a His residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          construction of an ALVAC-based recombinant virus containing a mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the wildtype human p53 gene from the translation initiation codon to the stop codon. This sequence was used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding cytokine and/or tumour associated antigen Example 32; Fig 39; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9416716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen; human; interferon; IFN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase chain reaction; poxvirus; pSD542; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human p53 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         067884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q67884 standard; DNA; 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or prostate carcinoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       form of the human p53 gene. The mutant form has a G>A substitution at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The wild-type p53 gene can be used in the production of a medicament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paoletti E, Tartaglia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1182 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 22;
Pred. No. 3.91e+00;
                                                                                                                                                                        Pred. No. 3.91e+00;
                                                                                                                                                                                                        Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                       0
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                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 C;
                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                       <u>,</u>
                                                                                                                                                                                                     Length 1182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1182;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                 0;
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ç В

1084 ageagggeteactecag 1100

26 AGCAGGGCTCACTCCAG 10

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Matches
              Best Local
                                                        colon carcinoma, lymphoma, leukaemia, etc., suggesting that mutation of the p53 genes is involved in oncogenesis. Specifically 273 Arg is replaced by 273 His, a mutation found exclusively in tumour cells. Sequence 1182 BP; 277 A; 368 C; 303 G; 234 T;
                                                                                                                       genes. Variant forms of p53 are found in human breast,
                                                                                                                                    cancers caused by defective, mutant or absent cancer suppressor
                                                                                                                                                 p53 cDNA, or its gene prods., can be used to suppress and eradicate
                                                                                                                                                               Claim 5; Page 15; 25pp; English.
                                                                                                                                                                                              neoplastic phenotype e.g. in osteo-sarcuma(s), leukaemia(s),
                                                                                                                                                                                                              Cloned p53 cDNA and protein prods. - for suppression of
                                                                                                                                                                                                                                               WPI; 92-090221/12.
                                                                                                                                                                                                                                                           Lee WH, Chen PL;
                                                                                                                                                                                                                                                                                           24-AUG-1990;
                                                                                                                                                                                                                                                                                                                                        EP-475623-A.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Cancer therapy; cancer suppressor gene; oncogenesis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1992 (first entry)
Sequence encoding 53 kD cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q22995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q22995 standard; DNA; 1182
                                                                                                                                                                                                                               P-PSDB; R22238.
                                                                                                                                                                                                                                                                          (REGC ) UNIV OF CALIFORNIA.
                                                                                                                                                                                                                                                                                                         23-AUG-1991;
                                                                                                                                                                                 lymphoma(s), etc.
                                                                                                                                                                                                                                                                                                                       18-MAR-1992
               h 56.7%;
Similarity 100.0%;
 Conservative
                                                                                                                                                                                                                                                                                         US-573405.
                                                                                                                                                                                                                                                                                                         307791.
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
              Pred. No. 3.91e+00;
                            Score 17;
<u>,</u>
  Mismatches
                            DB 3; Length 1182;
0;
 Indels
                                                                                                                       lung or
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Gaps
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ETT / LT COLOR TO COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia H6 promoter/human p53 expression cassette from vCP207.
Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53*tXbaISp6/T3; p53-21XbaI; p53-238XbaI;
                                                                                                                                                    /product= Wild type human p53
misc_feature 1415..1483
                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                  /note= "Vaccinia H6 promoter"
CDS 233..1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALVAC (CPpp) p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccinia; H6 promoter; plasmid; pRW825; expression cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q67864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q67864 standard; DNA; 1483
WO9416716-A.
                                            note= "Flanking sequence"
                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g sequence"
109..232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poxvirus; antigenic response; immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.7%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                             04-AUG-1994.
21-JAN-1994; U00888.
21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1994; U00888.
21-JAN-1993; US-007115.
19-JAN-1994; US-184009.
(VIRO-) VIROCENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccinia H6 promoter/human p53 expression cassette from vP1101.
Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant; human; p53; wild type; mutant; p53wtXbaISP6/T3; p53-21XbaI; p53-238XbaI; vaccinia; H6 promoter; plasmid; pRW825; expression cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q67863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1316 agcagggctcactccag 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI and p53-238XbaI respectively. The vaccinia H6 promotor was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53 gene. The expression cassettes generated by linking the vaccinia H6 promotor and the p53 genes may be cloned in to the poxvirus insertion plasmid, ALVAC, to give vCP207, vCP193 and vCP191 recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding cytokine and/or tumour associated antigen Example 15; Fig 18; 232pp; English.
                                                                                                                                                           /note= "Flanking sequence" W09416716-A.
                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                           misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALVAC (CPpp) p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q67863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viruses may be used in a composition for inducing an antigenic or immunological response, ie. for immunisation against pathogens. Sequence 1483 BP; 367 A; 415 C; 372 G; 329 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viruses, and into NYVAC to give vP1101, vP1096 and vP1098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mutant forms of the human p53 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               construction of poxvirus based recombinant viruses expressing wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in vP1101 and vCP207, respectively. These sequences were used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing the vaccinia H6 promoter and the wild type human p53 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in Q67863-64 represent expression cassettes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Attenuated recombinant virus used for cancer therapy - comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cox WI, Paoletti E, Tartaglia J; WPI; 94-263767/32.
                                                                                                                                                                                                                                                                                                                                                           SB
                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen; ss.
  (VIRO-) VIROGENETICS CORP
                                                                                                                                                                                                                                                                                            /product= Human
                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Vaccinia
                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 1512
                                                                                                                                                                                                                                                                                                                       a
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                                                                                                                                                                                                                                                                                                                                                     a H6 promoter"
269..1450
                                                                                                                                                                                                                                                              1451
                                                                                                                                                                                                                                                                                                                                                                                                                                               g sequence"
145..268
                                                                                                                                                                                                                                                                                   wildtype p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poxvirus; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 12; Length 1483; Pred. No. 3.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunological response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The wild type and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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AGACAGCAGGGCTCACTCCAG

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Mar 25 02:50 US-08-644-289-4 mg

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В ą В Matches Matches Best Local Query Match 56.7%; Best Local Similarity 100.0%; 8794 agacagcaaggcacactccag 1352 agcagggctcactccag of proteins and peptides, useful in the preparation of monoclonal and polyclonal HCV-specific antibodies.
Sequence 9502 BP; 1879 A; 2847 C; 2691 G; 2085 T; Claim 7; Pages 12-17; 35pp; Japanese. Q74770 encodes R66995 the HC-JI/protein, the cDNA can be used in the construction of an expression vector for the transformation. Q74770 plasmid, AIVAC, to give vCP207, vCP193 and vCP191 recombinant viruses, and into NYVAC to give vP1101, vP1096 and vP1098. The viruses may be used in a composition for inducing an antigenic immunological response, ie. for immunisation against pathogens. Sequence 1512 BP; 379 A; 419 C; 380 G; 334 T; DNA encoding cytokine and/or tumour associated antigen Example 15; Fig 17; 232pp; English.

The sequences given in Q67863-64 represent expression cassettes containing the vaccinia H6 promoter and the wild type human p53 gene in vP1101 and vCP207, respectively. These sequences were used in the construction of poxvirus based recombinant viruses expressing wild type 11-OCT-1994. 10-DEC-1993; Hepatitis C virus gene HC-J1/cDNA.
Hepatitis C virus; HCV gene HC-J1/cDNA; specific antibodies;
Hepatitis C virus. mutant genes were derived from plasmids p53wtXbaISP6/T3, p53-21XbaI and p53-238XbaI respectively. The vaccinia H6 promoter was derived from plasmid pRW825 and precisely linked to the 5'-most region of the p53 of a host cell. The host cell can then be used in the production HCV genes and the corresponding proteins - used in the production of anti-HCV antibodies and the detection of HCV infection P-PSDB; R66995. WPI; 94-362594/45. /\*tag= a J06284887-A. 01-AUG-1995 Q74770; promoter and the p53 genes may be cloned in to the poxvirus insertion and mutant forms of the human p53 gene product. The wild type and Attenuated recombinant virus used for cancer therapy -WPI; 94-263767/32: 10-DEC-1992; JP-360705 (IMMO ) IMMUNO JAPAN KK. 26 AGCAGGGCTCACTCCAG The expression cassettes generated by linking the vaccinia H6 standard; cDNA; 9502 Similarity 17; 19; Paoletti E, 345753 Conservative (first entry) Conservative Location/Qualifiers 56.7%; 90.5%; Tartaglia J; 8814 Pred. ВP Pred. No. 3.91e+00; Score 17; Score 17; DB 12; 0; <u>.</u> Mismatches Mismatches No. 3.91e+00; DB 13; 2; 0; Indels Length 1512; Length 9502; Indels comprises <u>.</u> 0 Gaps Gaps õ 0 0

Search completed: Tue Mar 25 02:52:51 1997 Job time : 15 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intellicenetics, Inc.

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Mar 25 02:51:15 1997; MasPar time 56.88 Seconds 434.390 Million cell updates/sec

Tabular output not generated.

Title: >US-08-644-289-4

Perfect Score: Description: (1-30) from US08644289.seq

N.A. Sequence: Comp: 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30 TCAGCCTAGGACCTCACTCGGGACGACAGA

Scoring table: TABLE default

Gap 10

Nmatch STD: Dbase 0; Query 0

Searched: 279077 seqs, 411808665 bases x 2

Post-processing:

Minimum Match 0% Listing first 45 summaries

embl-new5

Database: 1:BCT 2:FUN 3:INV1 4:INV2 5:ORG 6:MAM 7:VRT 8:PLN 9:PRI 10:PRO1 11:PRO2 12:ROD 13:SYN 14:UNC 15:VIR

Database:

16:BCT1 17:BCT2 18:BCT3 19:BCT4 20:BCT5 21:BCT6 22:BCT7 23:BCT8 24:BCT9 25:INV1 26:INV2 27:INV3 28:INV4 29:INV5 30:INV6 31:INV7 32:MAM1 33:MAM2 34:MAM3 35:VRT1 36:VRT2 37:VRT3 38:PAT1 39:PAT2 40:PAT3 41:PHG 42:PLM1 43:PLM2 44:PLM3 45:PLM4 46:PLM5 47:PLM6 48:PLM7 49:PLM8 50:PR11 51:PR12 52:PR13 53:PR14 54:PR15 55:PR16 56:PR17 57:PR18 56:PR19 59:PR110 60:PR111 61:PR112 62:PR113 63:ROD1 64:ROD2 65:ROD3 66:ROD4 67:ROD5 68:ROD6 69:ROD7 70:ROD8 71:STR 72:SYM 73:UMA 74:VRL1 75:VRL2 76:VRL3 77:VRL4 78:VRL5 79:VRL6 80:VRL7 81:VRL8 genbank 94

Database:

genbank-new5
82:BCT 83:INV1 84:INV2 85:MAM 86:VRT 87:PAT 88:PHG 89:PLN 90:PRI 91:ROD 92:STR 93:SYN 94:UNA 95:VRL u-embl46 94
96:partl

Database:

Statistics: Mean 7.318; Variance 2.910; scale 2.515

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	US-08-644-21
	US-08-644-28
	US-08-644-28
	US-08-644-289
	US-08-644-289-
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SUMMARIES

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17 17 17 17	17 17 17 17		18 17 17 17 17	21 21 21 21 21 21 21 18 18	22 22 21 21 21 21 21 21 21 21 21	Score
56.7 56.7 56.7 56.7 56.7	56.7 56.7 56.7	56.7 56.7 56.7 56.7	56.7 56.7 56.7 56.7		73.3 73.3 70.0 70.0 70.0 70.0 70.0 70.0	% Query Match
3127 3127 3127 3127 3680 5443 9502	1303 1650 1760 2066 2143 2143 2184		54336 54336 844 1179 1179 1179	1627 1772 1773 2130 2132 2132 1273 1273 136 2633 20303	3 4 4 4 7 8 4 O 2 5 I	Length
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MUSSDF1B MUSTLSFB MUSTLSFB HSU10692 HSG17G HPCHCJ1	HUMTP53B HUMTGKQL HUMP53T HSP53R CATP53 FCP53 MACP53A	HSP53004 HSP53008 HSP53003 HSP53007 HSP53009 HSP53002 HPCNS5J1	HUMXPDG1 HSXPDG1 DOGP53MUT HSP53010 HSP53006 HSP53005	MUSP53M MUSP53R MUSP53R MUSP53PG MMP53P RNU07019 HUMP53A10 RATTRKPREC HSP53G	RATP53TS07 MUSP53C MMANT10 MUSP53B MUSP53A MMP53 RATPSEUDO RATPSEUDO RAPSUEDO	ID
Mus musculus cytokine Mouse mRNA for TLAF-b Mouse thymic stromal Human MAGE-7 antigen H.saplens G17 gene. Hepatitis C virus gen		Human mRNA for mutate	sapiens ER sapiens ER familiari mRNA for mRNA for mRNA for	mkNA for e p53 cele mRNA foe mRNA foe mRNA foe e p53 cele pseudog us norveg n phosphous rattus n p53 gen	orveo	Description
5.32e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00		5.32e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00	1.13e+00 1.13e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00 5.32e+00	8.05e-03 8.05e-03 8.05e-03 8.05e-03 8.05e-03 4.36e-02 1.13e+00 1.13e+00		Pred. No.

#### ALI GNMENTS

RESULT 1						
Locus	RATP53TS07 159 bp	bp DNA		æ	ROD	14-JUL-1993
DEFINITION	Rattus norvegicus tumor suppressor (p53) gene, exon 9.	tumor sup	pressor (	p53)	gene,	exon 9.
ACCESSION	L07909 L07781					
NID	g205949					
KEYWORDS	tumor suppressor.					
SEGMENT	7 of 8					
SOURCE	Rattus norvegicus (strain Sprague-Dawley) DNA.	(strain S	prague-Da	wley)	DNA.	
ORGANISM	ORGANISM Rattus norvegicus					

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                            REFERENCE
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al Similarity 100.0%;
22; Conservation
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Mol. Cell. Biol. 6, 3232-3239 (1986)
                                                                                                                                                                                                                                                                                                            Rotter, V.
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                                                                                                                                                92253421
                                                                                                                                                           Nucleic Acids Res. 20, 1979-1981 (1992)
                                                                                                                                                                             different tissue types
                                                                                                                                                                                            Alternatively spliced p53 rRNA in transformed and normal cells
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                                                                                                                                                                                                                                                                                          Immunologically distinct p53 molecules generated by alternative
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/number=9
a 40 c
/gene="p53"
/map="11"
                                                            /organism="Mus musculus"
/cell_line="normal T-cell line L12"
/cell_type="Ab-MuLV transformed Meth A fibroblast"
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                                                                                                                              Location/Qualifiers
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/sequenced_mol="DNA"
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                                             /sequenced_mol="cDNA to mRNA"
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Pred. No.
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1.43e-03;
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Matches 21; Conservative
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MUSP53B
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LLPQDVEEFFEGE SEALMYSGAPAAQDEVTETPGEVAPAAPTPWLSSTYPSQKTYQG
NYGFHLGFLQSGTAKSVMCTYSPPLMKLFFQLAKTCPVQLMVSATPPAGSRVFAMAIY
KKSQHMTEVVRRCHHEECSDGDGLAPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE
PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG
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25 c 35 g
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                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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Pred. No. 1.43e-03;
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DEFINITION

COMMENT ç В FEATURES SOURCE ACCESSION DEFINITION **LOCUS** ORIGIN BASE COUNT FEATURES REFERENCE **EYWORDS** TITLE Matches MEDLINE JOURNAL AUTHORS ORGANISM Query Match 70.0%; Best Local Similarity 100.0%; 1183 agacagcagggctcactccag 1203 CDS source 30 AGACAGCAGGCTCACTCCAG 10 Eukaryotae; mitochondrial eukaryotee; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyee; Sarcopterygii; Choanata; g53570 X00741 MMP53 Data kindly reviewed (19-FEB-1986) by A. Wade-Evans Mus musculus Nucleic Acids Res. 12 (14), 5609-5626 (1984) encoding the transformation associated protein p53 Cloning and expression analysis of full length mouse Jenkins, J.R., Rudge, K., Redmond, S. and Wade-Evans, A. oncogene. Mouse mRNA 84272240 Sciurognathi; Myomorpha; Muridae; Murinae; Mus. Tetrapoda; Amniota; Mammalia; Theria; Eutheria; house mouse. 21; (bases 1 to 1377) 299 Conservative മ PPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPG RDRRTEEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTIKIRGRKR FEMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD\* 1..1377 NYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIY KSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEP /organism="Mus 123..1292 KKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYE LLPQDVEEFFEGPSEALRVSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQKTYQG /db\_xref="PID:g200199" /translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL /sub\_species="domesticus" /cell\_type="nontransformed helper T-cell" EMFRELNEALELKDAHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVKKVGPDSD" DRRTEEENFRKKEVLCPELPPGSAKRALPTCTSASPPQKKKPLDGEYFTLKIRGRKRF PEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGR YGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYK LLPRDVEEFFEGPSEALRVSGAPAAQDPVTETPGQWPAPATPWPLSSFVPSQKTYQGN translation="MTAMEESQSDISLELPLSQETFSGLWKLLPPEDILPSPHCMDDL/ /db\_xref="PID:g53571" /sequenced\_mol="cDNA to mRNA" /strain="BALB/ /codon\_start=1 /note="p53" Location/Qualifiers /product="p53 protein" codon start=1 113..1285 organism="Mus musculus" Location/Qualifiers for transformation associated protein p53. 1377 bp 385 c Score 21; DB 67; Pred. No. 8.05e-03; 0 334 g musculus" Mismatches 267 t <u>.</u> Length 1285; Indels Glires; Rodentia; 12-SEP-1993 <u>.</u> cDNA sequences Gaps <u>.</u>

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exon CDS	exon	exon misc_si	REFERENCE AUTHORS TITLE JOURNAL FEATURES source	RESULT 8 LOCUS DEFINITION ACCESSION NID NID KEYWORDS SOURCE ORGANISM	Best Local Matches  Db 1011 ag:	BASE COUNT ORIGIN	exon misc_si	exon	exon exon
	translation start site of the rat p53 cDNA; putation of the pseudogene corresponds to exhibit rat p53 cDNA; putative*	er"  of the pseudogene Nh; putative"	Lukaryota; Animalia; Chordata; verrebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  1 (bases 1 to 1447) 1 (bases 1 to 1447) Weghorst, C.M., Buzard, G.S., Hulla, J.E., Calvert, R.J. and Rice, J.M. Nucleotide sequence of a rat p53 pseudogene: a representative of the family of p53 pseudogenes in the rat genome Unpublished (1993) Location/Qualifiers 11447 /organism="Rattus norvegicus" /strain="Fisher 344" /screeneed fol="Num"	DNA ROD 07-3 tumor suppressor pseudogene, pa	al Similarity 100.0%; Pred. No. 8.05e-03; 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; agacagcagggctcactccag 1031	translation stop site of the rat p53 cDNA; putative" 366 a 388 c 336 g 357 t 70.0%; Score 21; DB 91; Length 1447;	321447  ote="this region of the pseudogene corresponds to of the rat p53 cDNA; putative" 071109 ote="this site within the pseudogene corresponds	/note="this region of the pseudogene corresponds to exon 8 of the rat p53 cDNA; putative" 9381031 /note="this region of the pseudogene corresponds to exon 9 of the rat p53 cDNA; putative"	of the rat p53 cDNA; 747882 /note="this region of of the rat p53 cDNA; 883937

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L12046;
16-MAR-1993 (Rel. 35, Created)
14-APR-1996 (Rel. 47, Last updated, Version 3)
Rattus norvegicus p53 (PG-III) pseudogene, partial
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                                                                                                                                                                                                                                                                                                              Weghorst C.M., Buzard G.S., Calvert R.J., Hulla J.E., Rice J.M.; "Cloning and sequence of a processed p53 pseudogene from rat: a potential source of false 'mutations' in PCR fragments of tumor DNA";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (rat)
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Eukaryota; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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1-1447
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of the rat p53 cDNA; putative"
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/db_xref="PID:g206473"
/translation="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDNQ
/translation="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDNQ
VCYVHVLPSPKLAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHWTEVMRRCSH
                                                                        /organism="Rattus norvegicus"
/strain="Fischer 344"
                                                                                                                                                                                                             Location/Qualifiers
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/tissue_type="liver"
                                         /sex="male"
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0; Mismatches 0;
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7 bp lear			rat pos 1109 *this si ation st A; 388 C	•,	"this re rat p53 1447	- 7 F-	at at	at hi	his at p	DQTPPP)	PSPKLA:	ef="PII	ial open	0		this			this:
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ein p53.		DB 1: 8.05e atches	putative hin the e of the G; 357 1	the	-	of the pa putativ	of the ps putativ		<b>+</b>	ଜୁ	CYVHVLPSPKLAILPAGEDMPCAVMGQLHTSNWHLCACHGIYKKSQHMTEVMRRCSHH	/coudi scalt=1 /db_xref="PID:g206473" /translation="KVQRKPSKCQLLPHRNLELRPLSLLKNLSQLWLSSGLPAVSDNQ	ng frame;	sor; this	of the pa putativ	-	site	outati in the	the
ROD		; Len 03; 0;	ve pseudogene cor e rat p53 cDNA; T; 0 other;	pseudogene	the pseudogene putative"	the pseudogene putative"	pseudogene Live"	the pseudogene putative*	the pseudogene		THANSLHT	HRNLELRP	e; putative;	is region	the pseudogene putative"	the pseudogene putative"	pseudogene of the rat p	tive"	seudogen
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                                         Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306, 594-597 (1983)
                                                                                                                                                                                                           DNA-binding protein; antigen; p53 gene; tumor antigen. Mouse embryo F9 carcinoma cells, cDNA to mRNA, clones p422, p208 [1], and clone pp53-1 [2].
                                                                                                                                                                                                                                                                                                                Mouse p53 cellular tumor antigen, mRNA. K01700
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                                                                                                                                                                  Eukaryota; Animalia; Chordata;
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(bases 105 to 1772)
                                                                                                             cheria; Rodentia; Myomorpha; (bases 1 to 1716)
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Pred. No. 8.05e-03;
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                                                                                                                                           Muridae; Murinae
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                                                                                                                                                                                                                                         clones p176, p271,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The murine p53 protein is similar to the avian and human myc gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid sequence of murine p53 determined from a cDNA clone Virology 134, 477-482 (1984)
                                               Mouse mRNA for cellular
X01237 K01700
                                                                                                                                                                                                                                                                                                                                                                                                          165 bp upstream of NcoI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There is only one functional p53 gene in the mouse genome. All existing different forms of murine p53 must be products of the same gene, mostly due to post-translational modifications [1]. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of cDNA in [1] was established by analysing four separate cDNA clones; p176 (bp 1-1247), p271 (bp 69-638), p422 (bp 1288-1719), and p208 (bp 1432-1719) [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins are rich in proline, contain proline runs or clusters, and are localized in the nucleus of tranformed cells. The Ela proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennica, D., Goeddel, D.V., Hayflick, J.S., Reich, N.C., Anderson, C.W.
antigen; tumor antigen.
                                                                                                    MMP53R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relative to the cDNA [1].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     products and the adenovirus Ela proteins. All three of these
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/map="11"
158..1330
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<1..1668</pre>
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Pred. No. 8.05e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zakut-Houri,R., Oren,M., Bienz,B., Lavie,V., Hazum,S. and Givol,D. A single gene and a pseudogene for the cellular tumour antigen p53 Nature 306 (5943), 594-597 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-NOV-1985) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bienz, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
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 /citation=[1]
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404
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al Similarity 100.0%;
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 MMP53P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 3.3-kb fragment isolated from a BALB/c genomic library, clone
                                                                                                                                                                                                                                                                                                                                                                                                                               the two sequences differ by only 4%. The differences are due to substitutions and to some small deletions or additions in this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide 186 onward. Upstream of this position the two sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     separate entry), and the psuedogene are almost identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The DNA sequence of pCh53-11 contains a long poly-A tract, lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84068204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                deverge totally and no homology can be observed; downstream of here
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of the murine p53 cDNA, also reported by [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from reverse transcription of the mature mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1852-1864), suggesting that it is a processed gene which resulted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pCh53-11.
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585 c 4
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                                                                                                                                                                                                                                                                                   /note="pseudo-p53"
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                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                       Score 21; DB 67; Length 2130; Pred. No. 8.05e-03; O; Mismatches 0; Indels
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Pred. No. 8.05e-03;
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Rodentia;

BASE COUNT ORIGIN FEATURES Best Matches exon CDS source Local ch 66.7%; 1 Similarity 88.5%; 23; Conservative 328 ۵ gene" /pseudo 359..539 /pseudo 24..1245 /pseudo 15..97 /clone="pR53P1" /strain="Wistar" /pseudo gene" /note="corresponds /gene="p53" /note="corresponds 888..961 641..750 540..640 98..119 /note="corresponds to a /tissue\_type="liver" organism="Rattus norvegicus" 962..1153 /note="corresponds /gene="p53" /note="corresponds /note="corresponds /cell\_type="hepatocyte" /sex="male" 154..>1273 'pseudo 'pseudo 'note="corresponds gene="p53" pseudo note="corresponds /gene="p53" 51..887 pseudo 'gene="p53" 'pseudo note="corresponds" 'gene="p53" pseudo note="corresponds /gene="p53" 20..358 'pseudo 'note="corresponds to exon 3 of the rat p53 gene" gene="p53" pseudo /gene="p53" ocation/Qualifiers 356 c Score 20; DB 70; I Pred. No. 4.36e-02; 0; Mismatches 3; 306 g to a ç ç ç ç ç to exon to exon 4 of ç exon exon exon exon exon exon 283 part of part of 6 10 9 of. ef. ٥f of ٥f of of. 3 Length 1273; exon the the exon 1 of the rat p53 the the the rat the rat the rat the Indels rat rat rat rat rat 11 of the rat p53 **p**53 **p**53 **p**53 **p**53 **p**53 **p**53 **p**53 p53 <u>.</u> gene" gene" gene" gene" gene" gene" Gaps <u>.</u>

망 1039 agacagcagggctcactcctgcctcc 1064

Department of Microbiology,

Myomorpha;

CP 30 AGACAGCAGGCTCACTCCAGGATCC 5

Search completed: Tue Mar 25 02:52:18 1997 Job time :  $63~{\rm secs}$  .

\* Œ

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\*

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Tue Mar 25 02:53:15 1997; MasPar time 56.30 Seconds 234.987 Million cell updates/sec

Run on:

Perfect Score: Description: Title: 30 (1-30) from US08644289.seq >US-08-644-289-4

N.A. Sequence: Comp: 1 AGTCGGATCCTGGAGTGAGCCCTGCTGTCT 30 TCAGCCTAGGACCTCACTCGGGACGACAGA

Scoring table: TABLE default

Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST27 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST25 23:EST23 32:EST33 32:EST33 32:EST33 33:EST33 34:EST34 35:EST35 36:EST36 31:EST31 32:EST38 33:EST37 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38 39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44 45:EST45 46:EST45 46:EST45 46:EST45 48:EST45 45:EST55 56:EST56 57:EST57 58:EST55 59:EST59 60:EST66 67:EST61 62:EST66 63:EST66 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68 69:EST69 70:EST70 77:EST77 72:EST72 73:EST73 74:EST74 75:EST75 76:EST76 83:EST88 89:EST89 90:EST99 91:EST99 92:EST99 93:EST99 94:EST98 95:EST96 97:EST97 98:EST98 99:EST99 9:EST9 10:EST10 EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 11:EST1 12:EST12 13:EST13 14:EST14

Database:

EST-STS-TWO

100:EST100 101:EST101 102:EST102 103:EST103 104:EST104 105:EST105 106:EST106 107:EST107 108:EST108 109:EST109 110:EST110 111:EST111 112:EST112 113:EST113 114:EST114 115:EST115 116:EST116 117:EST117 118:EST118 119:EST119 120:EST120 121:EST121 122:EST127 123:EST123 124:EST124 125:EST125 126:EST126 127:EST127 128:EST128 129:STS1

Mar 25 02:52

### US-08-644-289-4.rst

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7 136:STS8 137:STS9 138:STS10 139:ueEST 140:gnEST1 140:gnEST1 141:gnEST2 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 144:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 155:gnEST15 156:gnST15 157:enEST1 158:enEST2 159:enEST3 160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8 165:enEST9 166:enEST10 167:enEST11 168:enEST11 168:enEST11 169:enEST13 170:enEST14 171:enEST15 172:enEST16 173:enSTS1 174:enSTS2

Statistics: Mean 7.041; Variance 1.665; scale 4.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.

Score Match Length DB Query

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Description

Pred. No.

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RESULT LOCUS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens DNA. tetranucleotide repeat. KEYWORDS ACCESSION DEFINITION

microsatellite marker; sequence tagged site; PCR primer; STS sequence; microsatellite DNA; L30902

Human STS UT5411, HUMUT5411B

primer bind

STS

28-DEC-1994

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ALIGNMENTS

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Tocus

HUM030E06B

ACCESSION DEFINITION

D59424

g960530

HUM030E06B 303 bp mRNA E Human fetal brain cDNA 5'-end GEN-030E06.

303 bp

26-AUG-1995

KEYWORDS

EST(expressed sequence tag); Human fetal brain; similar to none(May 29,1995).
Homo sapiens (library: Clontech human fetal brain polyA+ mRNA

ORGANISM

Homo sapiens

(#6535)) cDNA to mRNA.

မှ B COMMENT RESULT ORIGIN BASE COUNT FEATURES REFERENCE SOURCE KEYWORDS ACCESSION Query Match 56.7%; Best Local Similarity 83.3%; Matches AUTHORS ORGANISM JOURNAL source 262 acagaagggctcactccncaatcc 285 28 ACAGCAGGCTCACTCCAGGATCC 5 w R12972 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Eucaryotae; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 295) Homo sapiens Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Contact: Wilson RK WashU-Merck EST Project Unpublished (1995) Wilson, R. Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., normalization. Library constructed by Bento Soares and M.Fatima the Lafmid BA vector. Library went through one round of Not I and directionally cloned into the Not I and Hind III sites of g766048 Source: IMAGE Consortium, LLNL High quality sequence stops: 233 Email: est@watson.wustl.edu Fax: 314 286 1810 GDB: G00-399-901 The WashU-Merck EST Project Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Bonaldo. human clone=27554 library=Soares infant brain 1NIB vector=Lafmid BA 20; This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 314 286 1800 78 Conservative മ /note="human" a 72 c /organism="Homo sapiens" /clone="27554" Location/Qualifiers Score 17; Pred. No. 8.05e-03; 0; Mismatches 59 g DB 75; 85 ~ 4. Length 295; Louis, 1 others Indels Homo. Gnathostomata; Mammalia; MO 63108 <u>.</u>. Gaps 0

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Best Local Similarity 62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
                                                                                                                                                                                                                                                                                                                    strain=W64A2 vector=ZipLox host=DH10B primer=T3 Reite1=SalI Rsite2=NotI ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zein.
Unpublished (1994)
                                                                                 Shen, B., Carneiro, N., Torres-Jerez, I., Helentjaris, T., Habben, J., Larkins, B.,
                                                                                                                                                                                                                                                                               strand to RNase-nicked DNA:RNA hybrid with DNA Poll. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            T18731
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Vartebrata: Sarcopteryqii; Mammalia; Eutheria; Primates;
                                          Single-Pass Sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                      Eucaryotae; Embryophyta; Magnoliophyta; Liliopsida; Cyperales;
                                                                                                                                                                                                                                   phage vector, excised as plasmids,
                                                                                                                                                                                                                                                         and size-selected. These were directionally-cloned into the ZipLox
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                                                              Baysdorfer,C
                                                                                                                                                    Poaceae; Zea.
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/clone_lib="Clontech human fetal brain polyA+ mRNA
(#6535)"
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Pred. No. 8.05e-03;
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                                                                               Stevenson, R., Almira, E., Ferl, R. and
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g879281
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                                                                                                                                                                                                                                          Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthy Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                       Source:
                                                                                                       High quality sequence stops: 310
                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                     Fax: 314 286 1810
                                                                                                                                                                                               4444 Forest Park Parkway,
                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                         Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                      Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of normalization to a Cot = 20. Library constructed by Bento Soares
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        digested with Not I and cloned into the Not I and Eco RI sites of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human clone=159293 library=Soares breast 3NbHBst vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MER22 repetitive element ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact:
                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                       Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and M.Fatima Bonaldo.
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                                                                                   IMAGE Consortium, LLNL
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Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
                                                                                                                                                                                                                                                                                                       Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
                                                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Assessment of Human Gene Diversity and Expression Patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
                                                                                                                                                       (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                 Email: tdbinfo@tdb.tigr.org
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/note="human"
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Best Local Similarity 90.0%;
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            za89b07.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 299701 5' similar to gb:L19067 TRANSCRIPTION FACTOR P65 (HUMAN); W05720
                                                                                                                                                                                                    ch 53.3%;
l Similarity 80.8%;
21; Conservative
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EST(expressed sequence tag).
Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toward an expression map of the C.elegans genome Unpublished (1995)
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g1278511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishigaki, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unpublished cDNA) Hermaphrodite embryo embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email:ykohara@ddbj.nig.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phone: 0559-81-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 Japan
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/tissue_type="embryo"
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Seq primer: mob.REGA+ET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the 
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                Sequence 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae
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                                                                                   C.elegans cDNA clone yk90h9 : 3' D72177
             Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara unpublished cDNA) Hermaphrodite embryo embryo cDNA to mRNA
Caenorhabditis elegans
                                                 EST (expressed sequence tag).
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                                                                                                                                                                                                                                                                             Pred. No. 1.00e-01;
                                                                                                                                                                                                                                                                                            Score 16; DB 164;
                                                                                                                                                                                                                                                           0; Mismatches
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;

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RESULT 11
LOCUS
DEFINITION
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Best Local Similarity 80.8%;
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                                                                                                                                                                                                                                                                                                                                                                          rat primer=M13 Reverse library=Rat PC-12 cells, untreated vector=pbluescript SK- Rsite1=EcoRI Rsite2=XhoI poly(A)+ RNA was purified from untreated PCl2 cells cultured for 9 days. cDNA was
                                                                                                                                                                   Fuldner,R.A., Marmaras,S., Glodek,A., Gocayne,J.D., Adams,M.D.,
Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                               Rattus sp.
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Kohara, Y., Motohashi, T., Tabara, H.,
                                            Contact: Lee NH
                                                                                                                          expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                Comparative expressed sequence tag analysis of differential gene
                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email:ykohara@ddbj.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
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                                                                                                       factor treatment
                                                                                                                                                                                                        Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A.
                                                                                                                                                                                                                                                   Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                   the Lambda ZAP II Vector Kit by Stratagene.
                                                                                                                                                                                                                                                                                                                                                        constructed using an oligo-dT primer and directionally cloned using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 Japan
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 Institute for Genomic Research Clopper Rd, Gaithersburg, MD 2
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/clone_lib="Yuji Kohara unpublished cDNA"
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Pred. No. 1.00e-01;
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Query Match 53.3%;
Best Local Similarity 80.8%;
Matches 21; Conservative
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Best Local Similarity 94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nhlee@tigr.org
For clone availability please contact
(tdbinfo@tdb.tigr.org).
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
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Caenorhabditis elegans (strain N2, ) (library: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.elegans cDNA clone yk51e7 : 3'
                                                                                                                                                                                                                                                                 Fax : 0559-81-6855
                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-Aug-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                             Toward an expression map of the C.elegans genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unpublished cDNA) Hermaphrodite embryo embryo
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                                                                                                                                                                                                                                                Email:ykohara@ddbj.nig.ac.jp.
                                                                                                                                                                                                                                                                                  Phone: 0559-81-6854
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                                                                                                                                                                                                                                                                                                 411 Japan
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                                                                                 /sex="Hermaphrodite"
/tissue_type="embryo"
/clone_lib="Yuji Kohara u
a 58 c 81 g 89
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Pred. No. 1.00e-01;
0; Mismatches 5;
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Pred. No. 1.00e-01;
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LOCUS CELK110HYR 329 bp mRNA
DEFINITION C.elegans cDNA clone ykl10h11 : 3'
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Best Local Similarity 94.4%;
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsona,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yf37b06.sl Homo sapiens cDNA clone 129011 3' R10375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis,
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Best Local Similarity 80.8%;
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                                                          Toward an expression map of the C.elegans genome
                                                                                  Nishigaki, A.
                                                                                                    Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
                                                                                                                                                  Rhabditidae; Caenorhabditis.
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Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
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/clone_lib="Yuji Kohara unpublished cDNA"
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complement component C2 gene, exon 10.			Bacillus subtilis DNA	Human DNA sequence		Caenorhabditis elegan	Caenorhabditis elegan	Caenorhabditis elegan Caenorhabditis elegan	Caenorhabditis elegan	Mouse P-cadherin gene	Pseudomonas fluoresce	S.cerevisiae chromoso	S.cerevisiae chromoso	Drosophila pseudoobsc			Drosophila pseudoobsc	Drosophila	Drosophila pseudoobsc Drosophila pseudoobsc	Drosophila		Drosophila pseudoobsc			Drosophila pseudoobsc	Drosophila	H.sapiens mRNA for sp STM=catecholamine-sul	Homo sapiens beta-1,6	Unidentified marine e	E.granulosus EgHbx2 h	Mouse complement comp	Description	SUMMARIES
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Statistics:

Mean 5.503; Variance 1.579; scale 3.486

RESULT 1

LOCUS MUSCCC210 1.53 bp DNA ROD DEFINITION Mouse complement component C2 gene, exon 10.

ACCESSION M60572 J05661

NID g192424

KEYMORDS complement component C2.

SECMENT 10 of 18
SOURCE Mouse DNA.

ORGANISM Mus musculus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryotae; mitochondrial eukaryotes; Taeniidae; Echinococcus.
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Submitted (12-JUN-1992) G.C. Oliver, Max-Planck-Inst of Biophysical Chemistry, Dept of Cell Biology, Am Fassberg 3400, Goettingen, FRG
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                                                                                                        Submitted (18-APR-1996) Vispo M., Dpto. Genetica. Facultad Biologia, Av. Diagonal 645, 08071 Barcelona, Spain E-mail:
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                                                                                      vispo@porthos.bio.ub.es
                                                                                                                                             Direct Submission
                                                                                                                                                              Vispo, M.
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/sequenced mol="DNA"
order(M60571:97..102,1..6)
/organism="Echinococcus granulosus"
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                                                                                                                                                                                                                                                                                                                      Submitted (21-NOV-1995) Stefan Weidner, Fakultaet fuer Biologie, Lehrstuhl fuer Genetik, Universitaet Bielefeld, Universitaetsstr. 25, Bielefeld, D-33615, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                    Halophila stipulacea estimated by restriction fragment length polymorphism analysis of PCR-amplified 16S rRNA genes Appl. Environ. Microbiol. 62 (3), 766-771 (1996)
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/product="165 ribosomal RNA"
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/note="associated with the seagrass Halophila stipulacea"
/clone="HstpL3" Location/Qualifiers /product="16S ribosomal RNA" 209 c' 296 g 199 t <1..>956 /note="related to 16S ribosomal 1..956 Location/Qualifiers marine 2060 bp eubacterium eubacterium Score 10; DB 82; Pred. No. 8.12e+02; <u>.</u> Germany Mismatches DB 82; Length 956; 0, RNAs from bacteria of the Indels 10-APR-1996 0; Ношо. Gaps 0;

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                                                                                                                                                                              NCBI
                                                                                                                                                                                                                                         Submitted (09-MAR-1995) A.J. Kramer, Universite de Geneve, Dept de Biologie Cellulaire, 30 quai Ernest-Ansermet, 1211 Geneve 4,
                                                                                                                                                                                                                                                                                                                                                                                    Kramer,A., Mulhauser,F., Wersig,C., Groning,K. and Bilbe,G. Mammalian splicing factor SF3al20 represents a new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                         Sequence overlapping with the
                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                          Kramer, A.J.
                                                                                                                                                                                                                                                                                                                                                       SURP family of proteins and is homologous to the essential splicing factor PRP21p of Saccharomyces cerevisiae
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                                                                 98..2479
                                                                                                                          /organism="Homo sapiens"
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/EC_number="3.2.1.23"
/note="NCBI gi: 899298"
/codon_start=1
                                  /gene="SF3a120"
                                                 /evidence=experimental
                                                                                chromosome="22"
                                                                                               /clone_lib="lambda gt11"
                                                                                                                /cell_line="HeLa"
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                                      NCBI gi: 833898
                                                                                                     catecholamine-sulfating phenol
                                                                                                                                                                                      Doggett N.A.;
                                                                                                                                                                                                                         Dooley T.P., Probst P., Munroe P.B.,
                                                                                                                                                                                                                                                                MEDLINE; 95100963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                               "Genomic organization and DNA sequence of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCATGCCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   backbone; DNA; PRI; 3225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /citation=[2]
2237..2467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SURP module 2" 857..901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RINVVPMPPSAPPIMAPRPPPMIVPTAFVPAPPVAPVPAPAPPAPPVHPPPPMEDEPTS
KKLKTEDSLMPEEEFLRRNKGPVSIKVQVPNMQDKTEWKLNGQVLVFTLPLTDQVSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDPKASKPLPPAPAPDEYLVSP1TGEKIPASKMQEHMRIGLLDPRWLEQRDRSIREKQ
SDDEVYAPGLDIESSLKQLAERRTDIFGVEETAIGKKIGEEEIQKPEEKVTWDGHSGS
MARTQQAAQANITLQEQIEAIHKAKGLVPEDDTKEKIGPSKPNEIPQQPPPPSSATNI
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ubiquitin-like domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593..721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVKTHEATGMPAGKQKLQYEGTFTKDSNSLAYYNMANGAVTHLALKERGGRKK'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSSAPP ITSVPRPPTMPPPVRTTVVSAVPVMPRPPMASVVRLPPGSVIAPMPP I IHAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQEKAEEPPSQLDQDTQVQDMDEGSDDEEEGQKVPPPPPETPMPPPLPPTPDQVIVRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDFVVVETVDFQPNEQGNFPPPTTPEELGARILIQERYEKFGESEEVEMEVESDEEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SF3a120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="charged domain"
1708..1892
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/db_xref="PID:g899298"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SF3a120"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="SURP module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SF3a120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MPAGPVQAVPPPPPVPTEPKQPTEEEASSKEDSAPSKPVVGII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                800 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10; DB 90;
Pred. No. 8.12e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679 g
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                                                                         sulfotransferase gene (STM)";
205:1325-1332(1994).
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                                                                                                                                                                                                                         Mole S.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tocas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                       ORGANISM
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promoter
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Sequence 3225 BP; 677 A; 940 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila pseudoobscura
                                                                                                                                                                                                                      Nucleotide sequence analysis of Adh genes estimates the time geographic isolation of the Bogota population of Drosophila
                                                                                                                                                                                                                                                                                                                                                                  alcohol dehydrogenase; alternative splicing.
Drosophila pseudoobscura (sub_species bogotana)
                                                                                                                                                                                                                                                                                                                                                                                                                     M60996
                                                                                                                                                                                                                                                       Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                      Drosophila pseudoobscura
                                                                                                                                                                                                                                                                                                                                                      EMBL4)
                                                                                                                                                                                                                                                                                                                                                                                                   g156855
                                                                                                                                                                                                                                                                                                                                                                                                                                    alcohol dehydrogenase (adh) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROADHBO39
                                                                                                                                                                                           Proc. Natl. Acad.
                                                                                                                                                                                                          pseudoobscura
                                                                                                                                                                                                                                                                                      Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                      Tracheata; Insecta; Pterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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Similarity 100.0%;
                                                                                                                                                                              .296768
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                                                                                                                                                          gi: 156855
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                                                                                                                                                                                                                                                                                                                                                      DNA.
                                                                                                                              1..3450
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                                                                              /tissue_lib="EMBL4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPKSGTTWVSQILDMIYQGGDLEKCNRAPIYVRVPFLEVNDPGEPSGLETLKDTPPPR
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2959,3082..3194)
  /codon_start=1
8..14
                                  /number=1
                                               /note="unidentified reading frame"
                                                                                               /sub_species="bogotana
                                                                                                            /organism="Drosophila
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKSHLP LALLPQTLLDQKVKVVYVARNPKDVAVSYYHFHRMEKAHPEPGTWDSFLEKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MELIQDTSRPPLEYVKGVPLIKYFAEALGPLQSFQARPDDLLIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="PID:e163343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Description: catecholamine-sulfating phenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="human"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3450 bp
                                                                                                                                                                                           Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10;
                                                                                                                                                                                          U.S.A. 88 (14), 6097-6101 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 8.12e+02;
                                                                                                              pseudoobscura"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                               bogotana, strain
                                                                                                                                                                                                                                                                                                                                                                                                                                    complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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/note="adult"
/number=1
2508..2912
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1467..1526
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TIAVNYTGLVNTTTA I LDFWDKRKGGPGGI I CNI GSVTGFNA I YQVPVYSGSKAAVVN
FTS SLAKLAP I TGVTAYTVNPGI TKTTLVHKENSWLDVEPRVAEKLLEHPTQTSQQCA
                              /gene="adh"
2207..2507
/note="unidentified reading frame"
                                                                               /note="potential"
1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="alcohol dehydrogenase"
893..998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
join(860..998,1062..1466,1527..1942)
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                                                                                                                                                                                                                                                                                                                                                                                           ENFVKAIELNKNGAIWKLDLGTLEPITWTQHWDSGI"
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join(893..998,1062..1466,1527..1942)
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/note="larval"
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                                                                                                                                  /codon_start=1
1919..1924
                                                                                                                                                                                                                                                                                                                          1062..1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSLTNKNVVFVAGLGGIGLDTSRELVKRNLKNLVILDRIDNPAA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="alcohol dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="NCBI gi: 156856"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /EC number="1.1.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="alcohol dehydrogenase"
join(906..998,1062..1466,1527..1793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="adh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="larval"
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120..892
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join(40..119,1062..1466,1527..1942)
                                                                                                                  /gene="adh"
                                                                                                                                                                    /number=3
                                                                                                                                                                                    'gene="adh"
                                                                                                                                                                                                                     'number=2
                                                                                                                                                                                                                                  /gene="adh"
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TITLE
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hes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROADHAH14 3463 bp DNA INV 07-MAY-1996 Drosophila pseudoobscura (strain AH144) alcohol dehydrogenase (adh)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila pseudoobscura
                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence analysis of Adh genes estimates the time of geographic isolation of the Bogota population of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 3463)
Schaeffer, S.W. and Miller, E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila pseudoobscura (tissue library: EMBL4) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alcohol dehydrogenase; alternative splicing
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                                                                                                                                                                                                                                                                                                                                                    NCBI gi: 156821
                                                                                                                                                                                                                                                                                                                                                                         91296768
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Pred. No. 8.12e+02;
0; Mismatches 0;
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NID Locus SOURCE ACCESSION DEFINITION KEYWORDS RESULT 10 g156823
alcohol dehydrogenase; alternative splicing.
Drosophila pseudoobscura (tissue library: EMBIA) DNA. M60985 Drosophila pseudoobscura (strain AH135) alcohol dehydrogenase (adh) gene, complete cds. DROADHAH15 3465 bp DNA ANI 07-MAY-1996

REFERENCE AUTHORS TITLE ORGANISM Schaeffer, S.W. and Miller, E.L. Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Ephydroidea; Drosophilidae; Drosophila. Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; (bases 1 to 3465)

MEDLINE JOURNAL Nucleotide sequence analysis of Adh genes estimates the time geographic isolation of the Bogota population of Drosophila 91296768 Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991) pseudoobscura of

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**BRNA** 

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exon

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> Mar 25 02:55 US-08-644-289-5.rge

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COMMENT DEFINITION FEATURES REFERENCE SOURCE KEYWORDS ACCESSION AUTHORS TITLE ORGANISM MEDLINE JOURNAI exon SG mRNA exon mRNA exon mRNA intron exon promoter source M60987 Drosophila pseudoobscura Nucleotide sequence analysis of Adh genes estimates the time of geographic isolation of the Bogota population of Drosophila 1 (bases 1 to 3466) Schaeffer, S.W. and Miller, E.L. Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. alcohol dehydrogenase; alternative splicing.
Drosophila pseudoobscura (tissue library: EMBL4) Drosophila pseudoobscura (strain AH162) alcohol dehydrogenase (adh) NCBI gi: 156825 g156825 91296768 Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991) pseudoobscura Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; DROADHAH16 complete cds. /gene="adh" /EC\_number="1.1.1.1" /product="alcohol dehydrogenase" join(926..1018,1082..1486,1547..1813) /codon\_start=1 join(913..1018,1082..1486,1547..1964) /gene="adh" /note="larval" /product="alcohol dehydrogenase" /codon\_start=1 join(880..1018,1082..1486,1547..1964) /codon\_start=1 join(40..119,1082..1486,1547..1964) note="adult" 'gene="adh" 'note="adult" 'gene="adh" 913..1018 number=1 note="larval" 880..1018 /note="adult" /product="alcohol 40..119 /note="adult" /codon\_start=1 /number=1 /note="unidentified reading frame" tissue\_lib="EMBL4" ′organism≃"Drosophila pseudoobscura" Location/Qualifiers note="NCBI gi: 156826" 'gene="adh" note="adult" 'gene≃"adh" 20..912 'gene="adh" 'note="adult" 'gene="adh" gene="adh" 3466 bp DNA dehydrogenase" ANI DNA. 07-MAY-1996

exon

intron

exon

intron

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Query Match 100.0%;
Best Local Similarity 100.0%;
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alcohol dehydrogenase; alternative splicing.
Drosophila pseudoobscura (tissue library: EMBL4) DNA.
Drosophila pseudoobscura
                                                                                                        Drosophila pseudoobscura (strain AH165) alcohol dehydrogenase (adh)
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    Mismatches

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exon

polyA\_site

polyA\_signal

Intron

NID

g156831

M60988

DEFINITION POCUS

12

DROADHAH 6

SOURCE

ORGANISM

/gene="adh" /number=2

084..1488

KEYWORDS ACCESSION မှ 밁

10 AGGCATGCCT 1

ORIGIN

Matches

BASE COUNT

973 a

polyA\_signal

exon

intron

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Nucleotide sequence analysis of Adh genes estimates the time of geographic isolation of the Bogota population of Drosophila  $\,$ 1 (bases 1 to 3467) Schaeffer, S.W. and Miller, E.L. NCBI gi: 156831 91296768 Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991) Ephydroidea; Drosophilidae; Drosophila. Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; pseudoobscura Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; /gene="adh" /number=1 /note="NCBI gi: 156832" /codon\_start=1 /product="alcohol dehydrogenase" /db\_xref="pID:g156832" /product=\*alcohol 915..1020 ENFVKAIELNKNGAIWKLDLGTLEPITWTQHWDSGI\* FTSSLAKLAP ITGVTAYTVNPGITKTTLVHKFNSWLDVEPRVAEKLLEHPTQTSQQCA IAELKA INPKVTITEYPYDVTVPVAETTKLLKTIFAQVKTIDVLINGAGILDDHQIER TIAVNYTGLVNTTTAILDFWDKRKGGPGGIICNIGSVTGFNAIYQVPVYSGSKAAVVN /gene="adh" /product="alcohol dehydrogenase" join(928..1020,1084..1488,1551..1817) /codon\_start=1 join(915..1020,1084..1488,1551..1966) /gene="adh" note="larval" /codon\_start=1 join(882..1020,1084..1488,1551..1966) /gene="adh" 882..1020 'gene="adh" /codon\_start=1 120..9<mark>14</mark> 40..119/number=1 join(40..119,1084..1488,1551..1966) /tissue\_lib="EMBL4" /organism="Drosophila pseudoobscura" 1..3467 Location/Qualifiers 021..1083 translation="MSLTNKNVVFVAGLGGIGLDTSRELVKRNLKNLVILDRIDNPAA EC\_number="1.1.1.1" note="adult" 'gene="adh" note="adult" number=1 'note="larval" 'gene="adh" 'note="adult" note="adult" 'gene="adh" 'product="alcohol note="adult" 'gene="adh" dehydrogenase" dehydrogenase"

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JOURNAL E MEDLINE COMMENT NE FEATURES Source	ORGANISM I	TION ION DS	Db 3331 ago	Query Match Best Local Matches	BASE COUNT ORIGIN (	exon polyA signal	intron	exon	porya_site	polyA_signal	exon	intron
Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6097-6101 (1991) 91296768 NCBI gi: 156851 Location/Qualifiers 13471	Dirosophila pseudoobscura Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Elavaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Dirosophila. 1 (bases 1 to 3471) 1 (bases 1 to 3471) Schaeffer, S. W. and Miller, E. L. Schae	DROADHBO35 3471 bp DNA INV 07-MAY-1996 Drosophila pseudoobscura (subsp. bogotana, strain BOG 3389.5) alcohol dehydrogenase (adh) gene, complete cds. M60994 g158851 alcohol dehydrogenase; alternative splicing. Drosophila pseudoobscura (sub_species bogotana) (tissue library: EMBI4) DNA.	aggcatgcct 3340           AGGCATGCCT 1	y Match 100.0%; Score 10; DB 83; Length 3467; Local Similarity 100.0%; Pred. No. 8.12e+02; hes 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/note="potential; unidentified reading frame" 980 a 793 c 786 g 908 t Chromosome IV, section 88.		/codon start=1 /codon start=1 29382995 /note="unidentified reading frame" /numbor=2 /numbor=2	/number=1 25332937 /note="unidentified reading frame" /note="unidentified reading frame" /number=2	/gene="adh" 2218.2532	āl	/number=2 /511966 /gene="adh" /number=3	/codon_start=1 intron 14891550 //eene="adh"

exon intron exon	intron	CDS	mRNA	exon	mRNA	exon	intron	mRNA	exon	promoter	exon
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exon	intron	polyA_site	polyA_signal		exon		intron		exon		intron							CDS			mRNA		exon			mRNA			exon	e xoo	intron		mRNA		exon	
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Drosophila pseudoobscura (strain AH100) alcohol dehydrogenase adh
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Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 8.12e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
polyA_signal
                                                                                                                      intron
                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                         polyA_site
                                                                                                                                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                        /gene="adh"
2229..2529
/note="unidentified r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAELKA INPKVTITFYPYDVTVPVAETTKLLKTIFAQVKTIDVLINGAGILDDHQIER
TIAVNYTGLVNTTTAILDFWDKRKGGPGGIICNIGSVTGFNAIYQVPVYSGSKAAVVN
FTSSLAKLAPITGVTAYTVNPGITKTTLVHKFNSWLDVEPRVAEKLLEHPTQTSQQCA
 /codon_start=1
3348..3353
                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="adh"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="adult"
/codon_start=1
join(928..1020,M60981:1084..1488,1549..1815)
/EC_number="1.1.1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
join(882..1020,1084..1488,1549..1964)
/gene="adh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENFVKAIELNKNGAIWKLDLGTLEPITWTQHWDSGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="NCBI gi: 1303659"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915..1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="alcohol dehydrogenase"
join(915..1020,1084..1488,1549..1964)
                                 /number=3
                                                 /note="unidentified reading frame"
                                                                   2993..>3353
                                                                                     /number=2
                                                                                                     note="unidentified"
                                                                                                                      2935..2992
                                                                                                                                                        number=2
                                                                                                                                                                        /note="unidentified reading frame"
                                                                                                                                                                                          2530..2934
                                                                                                                                                                                                          'number=1
                                                                                                                                                                                                                                                                              1964
                                                                                                                                                                                                                                                                                          note="potential"
                                                                                                                                                                                                                                                                                                               /gene="adh"
                                                                                                                                                                                                                                                                                                                               /codon_start=1
|941..1946
                                                                                                                                                                                                                                                                                                                                                               /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
1489..1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="adh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021..1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSLTNKNVVFVAGLGGIGLDTSRELVKRNLKNLVILDRIDNPAA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="alcohol dehydrogenase"
/db_xref="PID:g1303659"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="adh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="adh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="larval"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="larval"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="adh"
                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                'gene="adh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       084..1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="alcohol dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="adult"
                                                                                                                                                                                                                                                                                                                                                                                                 549..1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="adh'
                                                                                                                                                                                                                          reading frame"
                                                                                                     reading frame"
```

/note="potential; unidentified reading frame" BASE COUNT 967 a 793 c 800 g 912 t ORIGIN Chromosome IV, section 88.

ORIGIN Chromosome IV, section 88.

Query Match 100.0%; Score 10; DB 83; Length 3472;
Best Local Similarity 100.0%; Pred. No. 8.12e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Tue Mar 25 02:57:03 1997 Job time : 55 secs.

Db 3328 aggcatgcct 3337 ||||||||| Cp 10 AGGCATGCCT 1

1

١

Mar 25 02:55

US-08-644-289-5.mg

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intellicenetics, Inc.

\*

MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Twe Mar 25 02:57:21 1997; MasPar time 9.54 Seconds 91.416 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: 10 (1-10) from US08644289.seq >US-08-644-289-5

N.A. Sequence: Comp: 1 AGGCATGCCT 10 TCCGTACGGA

Scoring table: TABLE default Gap 10

Dbase 0; Query 0

Nmatch STD:

Searched: 113505 seqs, 43611913 bases x 2

Listing first 45 summaries

Post-processing: Minimum Match 0%

n-geneseq25
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 4.316; Variance 1.934; scale 2.231

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

O	ი	O				c		. Reg
<b>∞</b>	7	9	5	4	w	2	_	Result No.
10	10	10	10	10	10	10	10	sult No. Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
20	20	20	20	20	20	10	10	Query Match Length DB
19	5	21	5	21	19	5	5	
T10102	Q31978	T15968	Q31978	T15968	T10102	Q31948	Q31948	ID
Human cholecystokinin	Synthetic oligomer 4,	Primer for human CCK-	Synthetic oligomer 4,	Primer for human CCK-	Human cholecystokinin	Monomeric p53-specifi	Monomeric p53-specifi	Description
			1.99e+02		1.99e+02	1.99e+02	1.99e+02	Pred. No.

c	C	c	C				C	c			c		C		c		ი		n				o	a		O		G		ဂ		ဂ			
44	43	42	41	40	39	38	37	36	35	34	္ဆ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	=	10	9
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0			100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	•		100.0	100.0	100.0	100.0	100.0		•		100.0	100.0	100.0	100.0	100.0	100.0
4839 2	3353 1	3353 9											2272 20			-	1969 8	1969 8					831 14			91 9			-	42 13		~	24 8	24 20	
006827										Q56931	T14603	T14603	T11104	T11104	Q64563	Q64563	Q47671	Q47671	Q89201	Q89201	T16201	Q96290	Q79912	Q47710	Q47710	Q51746	Q51746	Q31 958	Q31 958	Q80759	Q80759	T11108	Q47714	T11107	T11108
Alpha amylase pullula Alpha amylase pullula	nce of ge	Amyloid precursor pro	e of human	precursor	Amyloid precursor pro	Sequence of gene enco	Insert DNA of pGP130	Human soluble glycopr	Insert DNA of pGP130		Ħ	Human gp130 native ge		Transforming growth f	В	K B rece	Sequence of the human		I-branching enzyme cD	I-branching enzyme cD	$\mathbf{a}$	Partial sequence of b		clone		Oligonucleotide probe	gonucleo.	binding		Pilot oligonucleotide	Pilot oligonucleotide	growth	e clone		Transforming growth f
1.99e+02 1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e + 02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e + 02	1.99e+02	1,99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02	1.99e+02

#### ALI GNMENTS

RESULATION RESULATION

Ş В 888888888888888 Matches Query Match Best Local Similarity various cancers. The construct may also be used to screen potential chemotherapeutic agents and to identify agents which specifically these sequences. Thus a function of p53 may be mediated by its ability to bind specific DNA sequences in the human genome. The sequence shown is a consensus sequence for p53 DNA binding. When inserted upstream and adjacent to a reporter gene the sequence restored to neoplastic cells having a mutation in their p53 genesee also Q31949-84. (UYJO ) UNIV JOHNS HOPKINS.
Kinzler KW, Sherman MI, Vogelstein B; P53; DNA-binding; cancer; neoplasia; tumour; ds. Q31948 standard; DNA; 10 BP restored to neoplastic cells having a mutation in their p53 gene. See also 031949-84. bind p53-specific DNA. Also wild-type p53 gene function may be allows identification of wild type p53, and such a construct could commonly found in human tumours do not have the ability to bind to bind p53-specific DNA. Also wild-type p53 gene function may be chemotherapeutic agents and to identify agents which specifically various cancers. The construct may also be used to screen potential be used for diagnosis of p53 mutations and onset and development of inserted upstream and adjacent to a reporter gene the sequence allows identification of wild type p53, and such a construct could ability to bind specific DNA sequences in the human genome. The sequence shown is a consensus sequence for p53 DNA binding. When these sequences. Thus a function of p53 may be mediated by viruses and animal cells. Four mutant forms of p53 protein which are commonly found in human tumours do not have the ability to bind to sequences are found near the origin of replication of certain animal stranded sequence shown separated by 0-13 base pairs. Wild-type p53 protein binds specific fragments of human chromosomal Claim 22; Page 24; 51pp; English. chemotherapeutic agents diagnosing and treating cancers, Detection and expression of wild type P53 protein - useful for WPI; 92-417505/51. (PHAR-) PHARMAGENICS INC. 31-MAR-1992; US-860758. 14-JUN-1991; US-715182. 10-JUN-1992; 305333 16-DEC-1992. EP-518650-A. Synthetic. Monomeric p53-specific DNA binding site. 27-APR-1993 (first entry) Q31948; Sequence be used for diagnosis of p53 mutations and onset and development of viruses and animal cells. Four mutant forms of p53 protein which are sequences are found near the origin of replication of certain animal l rrrcwwgyyy 10 1 AGGCATGCCT 10 Each tragment contains no more than one monomer of the double 2; 10 BP; Conservative 100.0%; 0 A; 0 A; Score 10; DB 5; I Pred. No. 1.99e+02; 1 C; 1 C; œ and Mismatches 1 G; . G; for screening 0 U; 0 U; 0; Indels Length 10; potential Some of these <u>,</u>, Gaps

> Mar 25 02:55 Matches Query Match 100.0%; Best Local Similarity 20.0%; 7 Conservative Score 10; DB 5; I Pred. No. 1.99e+02; US-08-644-289-5 mg 8; Mismatches 0; Indels Length 10; <u>,</u> Gaps 0

> > -

င့ 밁 10 AGGCATGCCT i 1 гггсимдууу 10

T10102 standard; DNA; 20 BP. T10102;

antagonist; gastric acid secretion; inhibition; anti-anxiety; ss. Cholecystokinin B; CCK-B; gastrin; receptor; human; isoform; Human cholecystokinin-B/gastrin receptor PCR primer. 17-JUL-1996 (first entry)

WPI; 96-065478/07. 30-MAY-1994; JP-117015. Synthetic. (YAMA ) YAMANOUCHI PHARM CO LTD. 30-MAY-1994; 117015. 12-DEC-1995.

0;

THE SOLPT IN THE S Cholecystokinin-B/gastrin receptor protein and gene - used to screen Example 2; Page 7; 14pp; Japanese. anti-anxiety agents and evaluate agents for use as gastric acid secretion inhibitors and

Query Match 100.0%; Best Local Similarity 100.0%; Cells transformed with the human coding sequence will express the receptor on their surface and will thus be useful for screening A cDNA sequence encoding the human isoform of cholecystokinin-B/ gastrin receptor was isolated (see T10094). The present sequence is that of a PCR primer which was used in cloning the full-length cDNA. candidate antagonists of the receptor. Such antagonists have anxiety agents. potential use as inhibitors of gastric acid secretion or as anti-20 BP; 4 A; Score 10; DB 19; Pred. No. 1.99e+02; 6 C; 4 G; 6 T; Length 20;

Ş В 7 aggcatgcct 16 1 AGGCATGCCT 10

Matches

10;

Conservative

0; Mismatches

<u>.</u>.

Indels

0

Gaps

0

ID ACC DIT DE KW KW KW PN PN PR PR PR PT PT PT PT TT gastric secretion; tranquilizer; assay; production; primer; PCR, 09-SEP-1996 (first entry)
Primer for human CCK-B/gastrin receptor gene amplification. CCK-B/gastrin; cholecystokinin-B/gastrin receptor; antagonist; develop antagonists used to evaluate inhibitors of gastric acid Gene encoding cholecystokinin-B/gastrin receptor - useful, e.g. to WPI; 96-136331/14. 22-JUL-1994; 170663. 22-JUL-1994; JP-170663. polymerase chain reaction; amplification; ss. T15968 standard; cDNA to mRNA; 20 30-JAN-1996. ло́8027190-А. Synthetic. (YAMA ) YAMANOUCHI PHARM CO O.L.1

secretion

US-08-644-289-5 mg

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8888888888888
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                                 В
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                                                                                   Best
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                                                                   Matches
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 7; 15pp; Japanese.
T15963-68 were used to PCR amplify a DNA fragment contg. a human cholecystokinin-B/gastrin receptor gene (see T15960). Host cells transformed with the gene are useful for recombinant production of the receptor protein. The receptor is useful for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q31978;
                                                                                                                                                                                   motif is required to bind p53, that G residues at nucleotides 4 and 6 are critical for p53 binding and that mutant p53 proteins found in tumours do not bind to the consensus sequence.
                                                                                                                                                                                                                                                                                                                       of 307 bp (range 139-470) was found. Only 18 of the clones contained unique fragments. Alignment of the inserts revealed a striking and
                                                                                                                                                                                                                                                                                                                                                                          Wild-type p53 protein binds specific fragments of human chromosomal DNA. 23 clones which bound p53 were obtd. by whole genome PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid secretion and tranquilizers, etc... Sequence 20 BP; 4 A; 6 C; 4 0
                                                                                                                                                                                                                                      binding.
                                                                                                                                                                                                                                                                       consensus sequence contains internal symmetry.
                                                                                                                                                                                                                                                                                         consistent feature, each binding site contained two copies of the 10\ \mathrm{bp}\ \mathrm{motif}\ 5'-\mathrm{RRRCWMGYYY-3'} separated by 0-13\ \mathrm{bp}. The 10\ \mathrm{bp}
                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Fig 10; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosing and treating cancers, and for screening potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinzler KW, Sherman MI, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-518650-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P53; DNA-binding; cancer; neoplasia; tumour; concatemer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic oligomer 4, to determine motif for binding to p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q31978 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical drugs, esp. antagonists to evaluate inhibitors of gastric
                                                                                                                                                    See also Q31948-84.
                                                                                                                                                                   Oligonucleotide 4 was capable of binding
                                                                                                                                                                                                                                                       were synthesised to determine portions of the motif vital for p53
                                                                                                                                                                                                                                                                                                                                                          The sequences of these 23 clones was compared and an average insert
                                                                                                                                                                                                                                                                                                                                                                                                                              chemotherapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection and expression of wild type P53 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAR-) PHARMAGENICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1992; US-860758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 100.0%;
Local Similarity 100.0%;
                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 aggcatgcct 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCATGCCT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92-417505/51.
 AGGCATGCCT 10
                                 aggcatgcct 10
                                                                                 h 100.0%;
Similarity 100.0%;
                                                                 10;
                                                                                                                                                                                                                                      Mutation analysis revealed that the dimer of the consensus
                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-715182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                    ₽₽;
                                                                                                                                 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뫈
                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.99e+02;
                                                                                                 Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                    6 C;
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; DB 21;
                                                                                   No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 G;
                                                                                                                                   6 G;
                                                                                                   DB 5;
                                                                                                                                                                      p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 T;
                                                                                                                                    4 T;
                                                                                                 Length 20;
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                         Synthetic oligomers
                                                                   Indels
                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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<del></del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
                                                 Wild-type p53 protein binds specific fragments of human chromosomal DNA. 23 clones which bound p53 were obtd. by whole genome PCR. The sequences of these 23 clones was compared and an average insert of 307 bp (range 139-470) was found. Only 18 of the clones contained unique fragments. Alignment of the inserts revealed a striking and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q31978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid secretion and tranquilizers, etc..
Sequence 20 BP; 4 A; 6 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer for human CCK-B/gastrin receptor gene amplification.
consensus sequence contains internal
                                                                                                                                        chemotherapeutic agents
Example 10; Fig 10; 51pp; English.
                                                                                                                                                                           diagnosing and treating cancers, and
                                                                                                                                                                                                                 WPI; 92-417505/51.
                                                                                                                                                                                                                                                 (PHAR-) PHARMAGENICS INC. (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                    14-JUN-1991; US-715182.
31-MAR-1992; US-860758.
                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic oligomer 4, to determine motif for binding to p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q31978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical drugs, esp. antagonists to evaluate inhibitors of gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transformed with the gene are useful for recombinant production of the receptor protein. The receptor is useful for the development of .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene encoding cholecystokinin-B/gastrin receptor - useful, e.g. develop antagonists used to evaluate inhibitors of gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1994; 170663.
22-JUL-1994; JP-170663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastric secretion; tranquilizer; assay; production; primer; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCK-B/gastrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-1996 (first entry)
                                    consistent feature, each binding site contained two copies of the
                                                                                                                                                                                             Detection and expression of wild type P53 protein - useful for
                                                                                                                                                                                                                                Kinzler KW, Sherman MI, Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                            EP-518650-A.
                                                                                                                                                                                                                                                                                                                                                                                           P53; DNA-binding; cancer; neoplasia; tumour; concatemer;
                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholecystokinin-B/gastrin receptor gene (see T15960). Host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase chain reaction; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T15968 standard;
                  10 bp motif 5'-RRRCWWGYYY-3' separated by 0-13 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YAMA ) YAMANOUCHI PHARM CO LTD.
WPI; 96-136331/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J08027190-A.
                                                                                                                                                                                                                                                                                                                         10-JUN-1992;
                                                                                                                                                                                                                                                                                                                                         .6-DEC-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [15963-68 were used to PCR amplify a DNA fragment contg. a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 7; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AGGCATGCCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 aggcatgcct 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholecystokinin-B/gastrin receptor; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 21;
Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                           for screening potential
 symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                  The 10 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
 oligomers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        motif is required to bind p53, that G residues at nucleotides 4 and 6 are critical for p53 binding and that mutant p53 proteins \frac{1}{2}
                                                                                        TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              candidate antagonists of the receptor. Such antagonist potential use as inhibitors of gastric acid secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cells transformed with the human coding sequence will express the receptor on their surface and will thus be useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide 4 was capable of binding p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastrin receptor was isolated (see T10094). The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A cDNA sequence encoding the human isoform of cholecystokinin-B/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and evaluate agents for use as gastric acid secretion inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholecystokinin-B/gastrin receptor protein and gene - used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 96-065478/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist; gastric acid secretion; inhibition; anti-anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholecystokinin B; CCK-B; gastrin; receptor; human; isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cholecystokinin-B/gastrin receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T10102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also Q31948-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         were synthesised to determine portions of the motif vital for p53
     DE19511243-A1
                                                            wound healing; polymerase chain reaction; PCR primer; ss.
                                                                                                                                                     Transforming growth factor beta cDNA clone MP-121 PCR primer LO2.
                                                                                                                                                                                    09-AUG-1996 (first entry)
                                                                                                                                                                                                                                           T11108 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anxiety agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that of a PCR primer which was used in cloning the full-length cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 7; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-anxiety agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1994; JP-117015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1994; 117015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J07324099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T10102 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found in tumours do not bind to the consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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                                                                                                                                                                                                                                                                                                                                                                                                7 aggcatgcct 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCATGCCT 1
                                                                                                                                                                                                                                                                                                                                       AGGCATGCCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Such antagonists have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                   by the cDNA insert has mitogenic and differentiation-inducing
                                        coding for a TGF-beta-like protein was isolated. The protein encoded
                                                                                                                                                               Example 1; Page 6; 15pp; German.
A cDNA library prepared using total RNA from human liver was
                                                                                                                                                                                                                                                                                                                               04-JAN-1996.
27-MAR-1995; 011243.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming growth factor beta cDNA clone MP-121 internal primer TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T11107 standard; cDNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing tissue regeneration. The present sequence is that of a PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by the cDNA insert has mitogenic and differentiation-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions within the TGF-beta family. Amplification products were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A cDNA library prepared using total RNA from human liver was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and differentiation-inducing activity, e.g. for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bechtold R,
properties making it (or fusion proteins comprising it or heterodimers
                                                             used to re-screen the human liver cDNA library and a 2272 bp fragment
                                                                                  to contain a new sequence. Part of the insert from this clone was
                                                                                                       subcloned and sequenced; one clone (designated pSK-MP121) was found
                                                                                                                           regions within the TGF-beta family. Amplification products were
                                                                                                                                        subjected to PCR amplification using primers corresp. to conserved
                                                                                                                                                                                                    and differentiation-inducing activity, e.g. for use in
                                                                                                                                                                                                                           DNA encoding transforming growth factor beta MP-121 - has mitogenic
                                                                                                                                                                                                                                                  WPI; 96-050788/06.
                                                                                                                                                                                                                                                                     Bechtold R,
                                                                                                                                                                                                                                                                                                              01-JUL-1994; DE-423190.
                                                                                                                                                                                                                                                                                                                                                                         DE19511243-A1.
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                              wound healing; polymerase chain reaction; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplification using primer LO2 (i.e. this sequence) and primer LOI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human liver library; positive clones were then subjected to PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              based on a DdeI fragment comprising nucleotides 931-1304 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding for a TGF-beta-like protein was isolated. The protein encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to re-screen the human liver cDNA library and a 2272 bp fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to contain a new sequence. Part of the insert from this clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subcloned and sequenced; one clone (designated pSK-MP121) was found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subjected to PCR amplification using primers corresp. to conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 6; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding transforming growth factor beta MP-121 - has mitogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 96-050788/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1994; DE-423190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1995; 011243.
                                                                                                                                                                                                                                                                                       (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2272 bp insert. The DdeI fragment was used as a probe to screen the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see T11109).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 aggcatgcct 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGCATGCCT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                   Neidhardt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neidhardt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 A;
                                                                                                                                                                                                                                                                   Pohl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pohl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 20;
Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                     Hoetten G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoetten G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                          wound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,;
                                                                                                                                                                                                        healing
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5

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RESULT
ID Q4
AC Q4
AC Q4
DT 11
DE TC
KW KW HC
KW C1
PF 1 1
RESULT
ID T.
AC T.
DT 0.
DE T.
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KW E.
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue regeneration. The present sequence is that of an internal primer which was used for isolating the cDNA coding sequence. Sequence 24 BP; 6 A; 5 C; 7 G; 6 T;
                                                    09-AUG-1996 (first entry)
Transforming growth factor beta cDNA clone MP-121 PCR primer IO2.
TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the protein with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encodes a protein which may be used in a pharmaceutical composition for the treatment of various bone, cartilage or tooth defects and in tissue and wound repair processes. These proteins may also be used as immunosuppressors in organ transplants and in cosmetic surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in 047711-14 are primers which may be used in the amplification of the liver derived human transforming growth factor-beta (TGF-beta) clone MP-121. The ampification product
  Synthetic.
                                                                                                                                                                                   T11108;
                                                                                                                                                                                                                T11108 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transforming growth factor-beta family proteins and DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoetten G, Neidhan WPI; 93-272824/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organ transplant; cosmetic surgery; antibody; diagnosis; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone; cartilage; tooth; wound repair; immunosuppressor; PCR; amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q47714 standard;
                             wound healing; polymerase chain reaction; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 13; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and tooth defects, and antibodies for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in tissue and wound repair, in treatment of bone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9316099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta-like clone MP-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-1992; EP-102324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-1993; E00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    8 aggcatgcct 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 aggcatgcct 17
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                                                                                                                                                                                                                                                                                                                                          AGGCATGCCT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raised against these proteins may be used for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neidhardt H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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                                                                                                                                                                                                                24 BP.
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5 C; 7 G; 6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal nested primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 8; L
Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.99e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 24;
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Mar 25 02:55 04-JAN-1996. DE19511243-A1. US-08-644-289-5.mg

မှ 밁 Matches Best Local Query Match by the cDNA insert has mitogenic and differentiation—inducing properties making it (or fusion proteins comprising it or heterodimers of the protein with a cystine knot motif protein) useful for inducing used to re-screen the human liver cDNA library and a 2272 bp fragment coding for a TGF-beta-like protein was isolated. The protein encoded subcloned and sequenced; one clone (designated pSK-MP121) was found to contain a new sequence. Part of the insert from this clone was subjected to PCR amplification using primers corresp. to conserved regions within the TGF-beta family. Amplification products were 27-MAR-1995; 011243. 01-JUL-1994; DE-423190. amplification using primer LO2 (i.e. this sequence) and primer LOI1 human liver library; positive clones were then subjected to PCR based on a DdeI fragment comprising nucleotides 931-1304 of the tissue regeneration. The present sequence is that of a PCR primer A cDNA library prepared using total RNA from human liver was Example 1; Page 6; 15pp; German. and differentiation-inducing activity, e.g. for use in wound healing DNA encoding transforming growth factor beta MP-121 - has mitogenic Bechtold R, (see T11109). Sequence 24 BP; 2272 bp insert. The DdeI fragment was used as a probe to screen the (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL. 10 8 aggcatgcct 17 AGGCATGCCT 1 Similarity 100.0%; 10; Neidhardt H, Conservative 100.0%; 6 A; Pohl Score 10; DB 20; Pred. No. 1.99e+02; 5 c; J, Mismatches Hoetten 7 G; ç 6 T; Length 24; Indels 0 Gaps 0

RESULT 08 AC Pilot oligonucleotide 30-12.

DNA-polymerase; DNAP; 5' nuclease; Thermus; DNA cleavage;
RNA cleavage; transcleavage; pilot oligonucleotide; hairpin; ss. Q80759; Q80759 standard; DNA; 42 BP 04-JUN-1993; US-073384. WO9429482-A. 06-JUN-1994; U06253 l9-JUL-1995 (first entry)

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Dahlberg JE,

Lyamichev VI;

hybridizes to substrate RNA. Sequence 42 BP; 8 A; substrate DNA to create a short hairpin with a stabilizing tetra-loop, and pilot oligonucleotide 30-0 (Q80760), which Disclosure: Page 98; 159pp; English.
The ability of a 5' nuclease to cleave a specific sequence. Brow MAD, Dahlber WPI; 95-036504/05. structure was tested using the pilot oligonucleotides 19-12 (given in Q80758) and 30-12 (Q80758), which hybridize to detection of specific target sequences. cleavage activity with reduced synthetic ability, used Nuclease(s) derived from thermostable DNA polymerase(s) eavage activity with reduced synthetic ability, used for have

12 C;

12 ç

10 T;

0

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Mar 25 02.55

US-08-644-289-5 mg

5

0

Ş DЬ Job time : 14 secs. Search completed: Tue Mar 25 02:57:35 1997 Matches Query Match 100.0%; Best Local Similarity 100.0%; Sequence consensus sequence contains internal symmetry. Mutation analysis revealed that the dimer of the consensus motif is required to bind p53 and that mutant p53 proteins found in tumours do not bind to the consistent feature, each binding site contained two copies of the 10 bp motif 5'-RRRCWWGYYY-3' separated by 0-13 bp. The 10 bp DNA. 23 clones which bound p53 were obtd. by whole genome PCR. chemotherapeutic agents Detection and expression of wild type P53 protein — useful for diagnosing and treating cancers, and for screening potential  ${\bf r}$ consensus sequence. See Sequence 46 BP; 6 A; unique fragments. Alignment of the inserts revealed a striking and of 307 bp (range 139-470) was found. Only 18 of the clones contained The sequences of these 23 clones was compared and an average insert Wild-type p53 protein binds specific fragments of human chromosomal Example 10; Fig 10; 51pp; English. Kinzler KW, Sherman MI, Vogelstein WPI; 92-417505/51. (PHAR-) (OLYU) 16 aggcatgcct 25 AGGCATGCCT 10 UNIV JOHNS HOPKINS. PHARMAGENICS 10; Conservative See also Q31948-84. Score 10; DB 5; L Pred. No. 1.99e+02; 16 C; 0; Mismatches В 6 G; 0; Indels Length 46; 18 T; 0; Gaps 0

\* \*\*\*\*\*\*\*\* (ME)

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MPsrch\_nn n.a. n.a. database search, using Smith-Waterman algorithm

Tabular output not generated.

Run on:

Tue Mar 25 02:57:55 1997;

MasPar time 54.05 Seconds 81.591 Million cell updates/sec

Description: Perfect Score: Title: 10 (1-10) from US08644289.seq >US-08-644-289-5

N.A. Sequence: Comp: 1 AGGCATGCCT 10 TCCGTACGGA

Scoring table: TABLE default

Gap

Nimatch

STD:

Dbase 0; Query 0

630489 seqs, 220513910 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

15.EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST27 22:EST22 23:EST23 24:EST26 25:EST25 26:EST26 27:EST27 28:EST28 24:EST28 23:EST28 24:EST40 41:EST41 42:EST42 43:EST43 44:EST44 44:EST44 44:EST44 48:EST44 49:EST45 56:EST56 57:EST57 58:EST55 55:EST55 54:EST56 67:EST56 66:EST66 67:EST67 68:EST66 63:EST68 46:EST64 65:EST65 66:EST66 67:EST67 68:EST68 66:EST67 77:EST77 77:EST77 77:EST77 78:EST78 79:EST78 76:EST76 78:EST78 78: 99:EST99 9:EST9 10:EST10 11:EST11 :EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8 12:EST12 13:EST13 14:EST14

Database:

EST-STS-TWO

100:EST100 101:EST101 102:EST102 103:EST103 104:EST104 105:EST105 106:EST106 107:EST107 108:EST108 109:EST109 110:EST110 111:EST111 112:EST112 113:EST113 114:EST114 115:EST115 116:EST116 117:EST117 118:EST118 119:EST119 120:EST120 121:EST121 122:EST122 123:EST123 124:EST124 125:EST125 126:EST126 127:EST127 128:EST128 129:ST51

130:STS2 131:STS3 132:STS4 133:STS5 134:STS6 135:STS7 136:STS8 137:STS9 138:STS10 139:weEST 140:gnEST1 141:gnEST1 142:gnEST3 143:gnEST4 144:gnEST5 145:gnEST6 146:gnEST7 147:gnEST8 148:gnEST9 149:gnEST10 150:gnEST11 151:gnEST12 152:gnEST13 153:gnEST14 154:gnEST15 152:gnEST13 153:gnEST14 154:gnEST2 159:enEST3 155:gnEST16 156:gnST5 157:enEST1 158:enEST2 159:enEST3 160:enEST4 161:enEST5 162:enEST6 163:enEST7 164:enEST8 165:enEST9 166:enEST1 168:enEST1 168:enEST9 166:enEST9 166:enEST1 168:enEST1 168:enEST9 166:enEST9 166:enEST1 168:enEST1 168:enEST9 166:enEST9 166:enEST1 168:enEST1 168:enEST9 166:enEST9 169:enEST13 170:enEST14 171:enEST15 172:enEST16 173:enSTS1 174:enSTS2

Statistics: Mean 5.340; Variance 0.849; scale 6.287

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match	7
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26	118	132	163	46	36	127	23	157	103	46	46	153	119	136	121	49	149	149	104	46	18	9	166	174	174	122	109	52	92	69	136	174	30	26	174	174	133	150	46	46	158	BB	
H64117	T61429	G10653	HS590321	HUM050C08B	H98640	T95171	н56900	AT 60221	RICS4377A	HUM051B03B	HUM047E12B	W21554	T67179	HUM4S1048	T75686	HUM518A03B	W10375	W10375	T06552	HUM064H04A	H40613	DY1B81C11	HS 909332	HSA061YG1	HSA061YG1	T77928	T28441	MUSGS01048	R71722	N46803	HSA3122C9	HSA312ZC9	HSCOEHO81	H65997	HSA244WH5	HSA244WH5	G11844	W14696	HUM052G06B	HUM052G06B	HS128324	ID	
yr57g04.rl Homo sapie	yc06a02.sl Homo sapie	human STS CHLC.UTR 03	zb69c09.sl Homo sapie	Human fetal brain cDN	yx12e06.s1 Homo sapie	ye39f07.rl Homo sapie	yr07b07.sl Homo sapie	F	cDNA, partial se	fetal brain cDN	brain cDN		Ното ѕар	Human chromosome 4 (c	10464 Arabidopsis tha	Human placenta cDNA 5	ma38c02.rl Soares mou	ma38c02.rl Soares mou	EST04441 Homo sapiens	Human fetal brain cDN	Homo sa	H. sapiens partial cD	1 Soares pa	(D3S3711)	H.sapiens (D3S3711) D	yd16f05.rl Homo sapie	1578	Mouse 3'-directed cD						Homo sapie	(D1S2675)	(D1S267	WI-10852	05.rl	fetal	l brain c	za96h06.rl Soares fet	Description	
2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	2.46e+01	4	2.46e+01	Pred. No.								

mb45g09.rl Soares mou

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#### ALIGNMENTS

HS128324

standard; RNA; EST;

205 BP

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44 45

10 10

Matches Query Match 100.0%; Best Local Similarity 100.0%; School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., za96h06.rl Soares fetal lung NbHL19W Homo sapiens cDNA clone 300443
5' similar to contains LTR5.t3 LTR5 repetitive element ;. Key Hillier L., 27-APR-1996 (Rel. 47, Created) 27-APR-1996 (Rel. 47, Last, updated, W07128; Sequence source stop: 110. NCBI gi: 1281421 further information. Seq primer: mob.REGA+ET High quality sequence Contact: Wilson RK WashU-Merck EST Project Washington University Unpublished Theria; Eukaryota; Homo sapiens (human) LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) "The WashU-Merck EST Project"; Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; ta; Animalia; Metazoa; Chordata; Eutheria; Primates; Haplorhini; 10; 205 B₽; Conservative /clone\_lib="Soares fetal lung NbHL19W" /dev\_stage="19 weeks" /lab\_host="DH10B (ampicillin resistant)" Soares and M.Fatima Bonaldo. This library was constructed normalization to a Cot = 5. Library constructed by Bento adapters (Pharmacia), digested with Not I and cloned into /clone="300443" fetal heart NbHH19W. (Pharmacia). Library went through one round of the Not I and Eco RI sites of a modified pT7T3 vector /organism="Homo sapiens" 58 A; 49 C; 53 G; 42 T; 3 other; from the same fetus as the fetal heart library, Soares Location/Qualifiers Score 10; DB 158; Pred. No. 2.46e+01; **.** Mismatches Version 1) ; Vertebrata; ; Catarrhini; 0 Length 205; Indels Mammalia; Hominidae. Marra M., for <u>.</u> Gaps 0;

S 밁 71 aggcatgcct 80 AGGCATGCCT 10

> Mar 25 02:57 US-08-644-289-5 rst

RESULT Ş 밁 Locus FEATURES COMMENT REFERENCE REFERENCE Ü TOCUS SOURCE KEYWORDS ACCESSION DEFINITION BASE COUNT SOURCE KEYWORDS ACCESSION DEFINITION ORGANISM Matches Query Match 100.0%; Best Local Similarity 100.0%; AUTHORS AUTHORS ORGANISM JOURNAL JOURNAL source 129 aggcatgcct 138 <u>--</u> AGGCATGCCT 10 D80249 HUM052G06B 239 bp mRNA E Human fetal brain cDNA 5'-end GEN-052G06. Homo sapiens Human fetal brain cDNA 5'-end GEN-052G06 Homo sapiens Fetus brain cDNA to mRNA, clone\_lib:human fetal brain. EST(expressed sequence tag); Human fetal brain. g1178126 HUM052G06B 463-10 Kagasuno Kawauchi-cho 0tsuka Otsuka Unpublished (1995) Maekawa, H., Shin, S. and Nakamura, Y. Okuno, S., Ozaki, K., Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Direct Submission Fujiwara, T. D80249 Vertebrata; Eutheria; Primates; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; 10; Fax :0886-37-1035 Phone:0886-65-2888 771 - 01Tokushima, Tsutomu Fujiwara Submitted (7-Nov-1995) to DDBJ Large-scale sequencing project at Otsuka GEN Research Institute Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Japan Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; (bases 1 to 239) (bases 1 to 239) 65 Conservative Pharmaceutical CO., Ltd GEN Research Institute /organism="Homo sapiens"
/sequenced\_mol="cDNA to mRNA"
/tissue\_type="brain"
58 c 55 g 44 t 1..239 /dev\_stage="Fetus" /clone\_lib="human fetal brain" Location/Qualifiers Tokushima 239 bp Shimizu, F., Pred. No. 2.46e+01; Score 10; **.**: IIRNA Mismatches by: DB 46; Shimada, Y., Shinomiya, H., Catarrhini; Hominidae; 0 Length 239; 17 others Indels 18-DEC-1995 18-DEC-1995 Hirai, Y., 0 fetal brain. Gaps 0

REFERENCE

TITLE

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AUTHORS

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129 aggcatgcct 138
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Local Similarity 100.0%;
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                      g1288727
                                                                                                                                                                                                                                                                                                                                                                                                                                mb34g05.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 331352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                W14696
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Unpublished (1996)
                                               Theising,B., Wylie,T., Lennon,G., Soares,B., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phone: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463-10 Kagasuno Kawauchi-cho
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                                                                                                                                                                                                                         Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                          The WashU-HHMI Mouse EST Project
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Pred. No. 2.46e+01;
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ORIGIN BASE COUNT

Best

Matches Query Match

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FEATURES

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COMMENT

Whitehead Institute/MIT Center for Genome Research

Contact: Thomas Hudson

TITLE

JOURNAL

REFERENCE

AUTHORS

SOURCE KEYWORDS ACCESSION DEFINITION **LOCUS** RESULT

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ORGANISM

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Best Local Similarity 100.0%;
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                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                               STS sequence; primer; sequence tagged site. human STSs derived from random genomic DNA.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Unpublished (1995)
                                                                          Hudson, T.
                                                                                                                                 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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                                   Mapped STSs
                                                       Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                                 Catarrhini; Hominidae; Homo.
                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into
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/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                              269 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10; DB 150;
Pred. No. 2.46e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                                                                                                                                                    STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                19-0CT-1995
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RESULT
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                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                     Matches
HSA244WH5 standard; DNA; STS; 272 BP.
252679;
18-MAR-1996 (Rel. 47, Created)
23-MAR-1996 (Rel. 47, Last updated, Version 3)
H.sapiens (D152675) DNA segment containing (CA) repeat; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                   primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prepared with primer pairs derived from random genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer B: TCAATCCTACTGGGAATTTCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer A: TTCTCTGATGCTAGGGTAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
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                                                                                                                                                                                                                                                   Conservative
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Polymerization:
PCR Cycles: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermal Cycler:
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                                                                                                                                                                                                                                                                                                                                         complement (246..269)
/map=*746_D 8; 854_E_5; 891_G_9; 950_G_3; 950_G_4;
747_D 11; 811_D 12; 838_C_10; 854_E_10; 870_G_10; 730.7 cR
from top of Chrl linkage group*
a 73 c 66 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="746_D_8; 854_E_5; 891_G_9; 950_G_3; 950_G_4; 747_D_11; 811_D_12; 848_C_10; 854_E_10; 870_G_10; 730.7 from top of Chrl linkage group"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                               Score 10; DB 133; Length 269; Pred. No. 2.46e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 Indels 0;
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repeat; GT repeat; I
Homo sapiens (human)  Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
1-272 Weissenbach J.;
; Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases. Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: Jean.Weissenbach@genethon.fr Jean.Weissenbach@genethon.fr
1-272  Dib C., Faure S., Fizames C., Samson D., Drouot N., Vignal A., Millasseau P., Marc S., Hazan J., Seboun E., Lathrop M., Gyapay G., Morissette J., Weissenbach J.; Gyapay G., Morissette J., Weissenbach J.; A comprehensive genetic map of the human genome based on 5.264
prosatellites"; ture 380:152-154(1996). Il automatic; Location/Qualifiers
source 1272 /organism="Homo sapiens" /cell_line="CEPH 134702" /clone_lib="genomic DNA" /chromosome="1" /note="cloning vector is M13mp18" Sequence 272 BP; 82 A; 79 C; 64 G; 44 T; 3 other;
uery Match 100.0%; Score 10; DB 174; Length 272; est Local Similarity 100.0%; Pred. No. 2.46e+01; atches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
141 aggcatgcct 150            :: 1 AGGCATGCCT 10
standar (Rel. (Rel. ) (Rel. )
Armazyawni); Single read.  CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS.  Homo sapiens (human)  Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
Weissenbach J.; ; Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases. Genethon, B.P. 60, 91002 Evry Cedex France. E-mail: Jean.Weissenbach@genethon.fr [2]
1-2/2 Dib C., Faure S., Fizames C., Samson D., Drouot N., Vignal A., Millasseau P., Marc S., Hazan J., Seboun E., Lathrop M.,

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 272 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 aggcatgcct 150
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        н65997
                                                                                                                                                                                                                                                                                                                               Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H65997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yr73c10.r1 Homo sapiens cDNA clone 210930
                  Email: estewatson.wustl.edu
High quality sequence stops: 189
Source: IMAGE Consortium, LLNL
                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA was primed with a Pac I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and spleen from a 20 week-post conception male fetus. 1st strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver
                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                              WashU-Merck EST Project
                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                             Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Archonta; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human clone=210930 primer=M13RP1 library=Soares fetal liver spleen
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 290)
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ensive genetic map of the human genome based on 5,264
                                                                                                                              Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="cloning vector is M13mp18"
82 A; 79 C; 64 G; 44 T; 3 other;
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/cell_line="CEPH 134702"
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Pred. No. 2.46e+01;
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                  expression
C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
Clone library from B.Soares, Psychiatry Dept. Columbia University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. sapiens partial Z42301
                                             Stretch_removed: nothing Normalization_method: Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Genexpress cDNA program Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
                                                                                                                                                                                   Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' \rightarrow 3' into the HindIII \rightarrow NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                             Auffray, C., Behar, G., Bois, F., Boucher, C., da Silva, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g565710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE
Genexpress_sequence_idt: y1c-0eh08;
                         Genexpress_library_idt: C;
                                                                                           cDNA sequence colinear to mRNA
                                                                                                                  Primer: M13_reverse
                                                                                                                                   Sequencing_method: single read,
                                                                                                                                                                                                                                                                                                                                         IMAGE: Integated molecular analysis of the human genome and its
                                                                                                                                                                                                                                                                                                                                                              Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                                                                                        Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 292)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSC0EH081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 292)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1..>290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/clone="210930"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence; clone c-0eh08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10; DB 26;
Pred. No. 2.46e+01;
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                                                                                                                                         full automatic;
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                                                  P.N.A.S
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No sign. genbank

significant homology found with :

release 81 swissprot release

28

Location/Qualifiers

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Best Local Similarity 100.0%;
Matches 10; Conservative
               Best
  Matches
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Z52895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1996 (Rel. 47, Last updated, Version H.sapiens (D1751818) DNA segment containing AFMa312zc9; single read.
                                                                                                                                                                                                                                             Millasseau P., Marc S., Hazan J., Seboun E., Lathrop M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                     source
                                                                                                                                                                                                          microsatellites
                                                                                                                                                                                                                                 Gyapay G., Morissette J., Weissenbach J.;
                                                                                                                                                                                                                                                              Dib C., Faure S., Fizames C., Samson D., Drouot N., Vignal A.,
                                                                                                                                                                                                                                                                                                                                 Submitted (01-SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            Weissenbach J.;
                                                                                                                                                                                                                                                                                                                                                                                                      Theria; Eutheria; Primates; Haplorhini; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                             microsatellite marker; repeat polymorphism; STS.
                                                                                                                                                                                            Nature 380:152-154(1996).
                                                                                                                                                                                                                                                                                                      Genethon, B.P. 60, 91002 Evry Cedex France. E-mail:
Jean.Weissenbach@genethon.fr
                                                                                                                                                                                                                    A comprehensive genetic map of the human genome based on 5,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8-MAR-1996 (Rel. 47, Created)
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           y Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /isolate="muscular atrophy patient"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
                                                  /note="cloning vector is M13mp18" 65 A; 98 C; 45 G; 81 T; 6 other;
                                                                                /chromosome="17"
                                                                                             /clone_lib="genomic DNA"
                                                                                                          /organism="Homo sapiens"
/cell_line="CEPH 134702"
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="3 months old"
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           Score 10; DB 174;
Pred. No. 2.46e+01;
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Pred. No. 2.46e+01;
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Mismatches
                         DB 174; Length 295;
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yy52e05.rl Homo sapiens on N46803
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSA312ZC9 295 bp DNA STS H.sapiens (D1751818) DNA segment containing
                                                                 human clone=277184 primer=T7 library=Soares multiple sclerosis 2NbHMSP vector=pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid host=DH10B (ampicillin resistant) Rsitel=Not I Rsite2=Eco RI 46 year old male. 1st strand cDNA was primed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-SEP-1995) Genethon, B.P. E-mail: Jean.Weissenbach@genethon.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS.
                                A comprehensive genetic map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Millasseau, P., Marc, S., Hazan, J., Seboun, E., Lathrop, M., Gyapay, G., Morissette, J. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dib, C., Faure, S., Fizames, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
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                 double-stranded cDNA was size selected,
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 380, 152-154 (1996)
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/cell_line="CEPH 134702"
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98 c 45
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   digested with Not I and cloned
                                                                                                                                                                                                        309 bp
                                                                                                                                                                                                                                                                                                                                                                Score 10; DB 136;
Pred. No. 2.46e+01;
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                                                                                                                                                                                        cDNA clone 277184
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ligated to Eco RI adapters oned into the Not I and Eco
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                                                                   cDNA was primed with a
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US-08-644-289-5.rst

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RESULT 13
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DEFINITION
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JOURNAL
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Best Local Similarity 100.0%;
Matches 10; Conservative
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15576 אין אַריע אַרָּר אַרָּאָרָר אַרָּאָר אַרָּאָרָר אַרָּאָר אַרָּאָר אַרָאָר אָרָאָר אָרָאָר אָרָאָרייייי
                double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 230. Library constructed by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RI sites of a modified pTTT vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library
                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Soares and M.Fatima Bonaldo
                                                                                                                                                                                                                                                                          g845754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stops: 25
Source: IMAGE Consortium, LINL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project 
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis lesions from one patient was kindly provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 314 286 1810
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/clone="277184"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10; DB 60;
Pred. No. 2.46e+01;
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RESULT 14 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES  FEATURES  SOUTCE  BASE COUNT ORIGIN  Query Match Best Local Matches  Db 220 agg         Qy 1 AGG	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS
MUSGS01048 313 bp mRNA EST 09-DEC-1995 MOUSE 3'-directed cDNA, MUSGS01048, clone mc0750.  D18866 g1089499 EST(expressed sequence tag); Gene signature(GS); development; transcribed sequence. Mus musculus (strain C57BL/6Jsub species domesticus, ) decidual tissue (day 6.5-8.5 of gestation) cDNA to mRNA.  Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus. 1 (bases 1 to 313) Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K. Analysis of gene expression in mouse embryogenesis by3'-directed cDNA sequencing Unpublished (1993) Submitted (10-Sep-1993) to DDBJ by: Shoko Kawamoto Institute for Cellular and Molecular Biology Osaka University	Fax: 314 286 1810  Email: estewatson.wustl.edu High quality sequence stops: 189 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers 1.311 /organism="Homo sapiens" /clone="15576" /clone="15576" /clone="15576" /note="human" 69 a 101 c 63 g 74 t 4 others  ttch 100.0%; Score 10; DB 92; Length 311; al Similarity 100.0%; Pred. No. 2.46e+01; 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; aggcatgcct 229                AGGCATGCCT 10	., Waterston,R., Williamson,A., Wohl erck EST Project (1995) lson RK EST Project University School of Medicine Park Parkway, Box 8501, St. Louis, 6 1800	Homo sapiens  Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;  Buterostomia; Chordata; Verrebrata; Gnathostomata; Osteichthyes;  Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria;  Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 311)  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  Parsons, J., Riffin, L., Rohlfing, T., Soares, M., Tan, F.

Phone: 06-879-7992 Suita, Osaka, 565

Japan

3-1, Yamadaoka

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Best Local Similarity 100.0%;
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                                                                                                                                                                                            EST44578 Homo sapiens cDNA 5' end similar to
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                            Unpublished (1995)
                                                                                                                             Based Upon 52 Million Basepairs of cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Kelley, J.M., Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                             FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S. Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
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                                                                                                                                                                              Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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                                                                                                                                                    Initial Assessment of Human Gene Diversity and Expression Patterns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax : 06-877-1922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
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Mar 25 02:57 US-08-644-289-5 rst

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Email: tdbinfo@tdb.tigr.org Fax: 3018699423

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org). Location/Qualifiers

FEATURES

source

<1..>313 /organism="Homo sapiens" /note="human"

mRNA BASE COUNT ORIGIN 64 c 65 g 100 t

Matches Query Match 100.0%; Best Local Similarity 100.0%; 10; Conservative Pred. No. 2.46e+01; Score 10; 0; Mismatches DB 109; Length 313; Indels <u>.</u> Gaps

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Job time : 62 secs Search completed: Tue Mar 25 02:58:57 1997

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